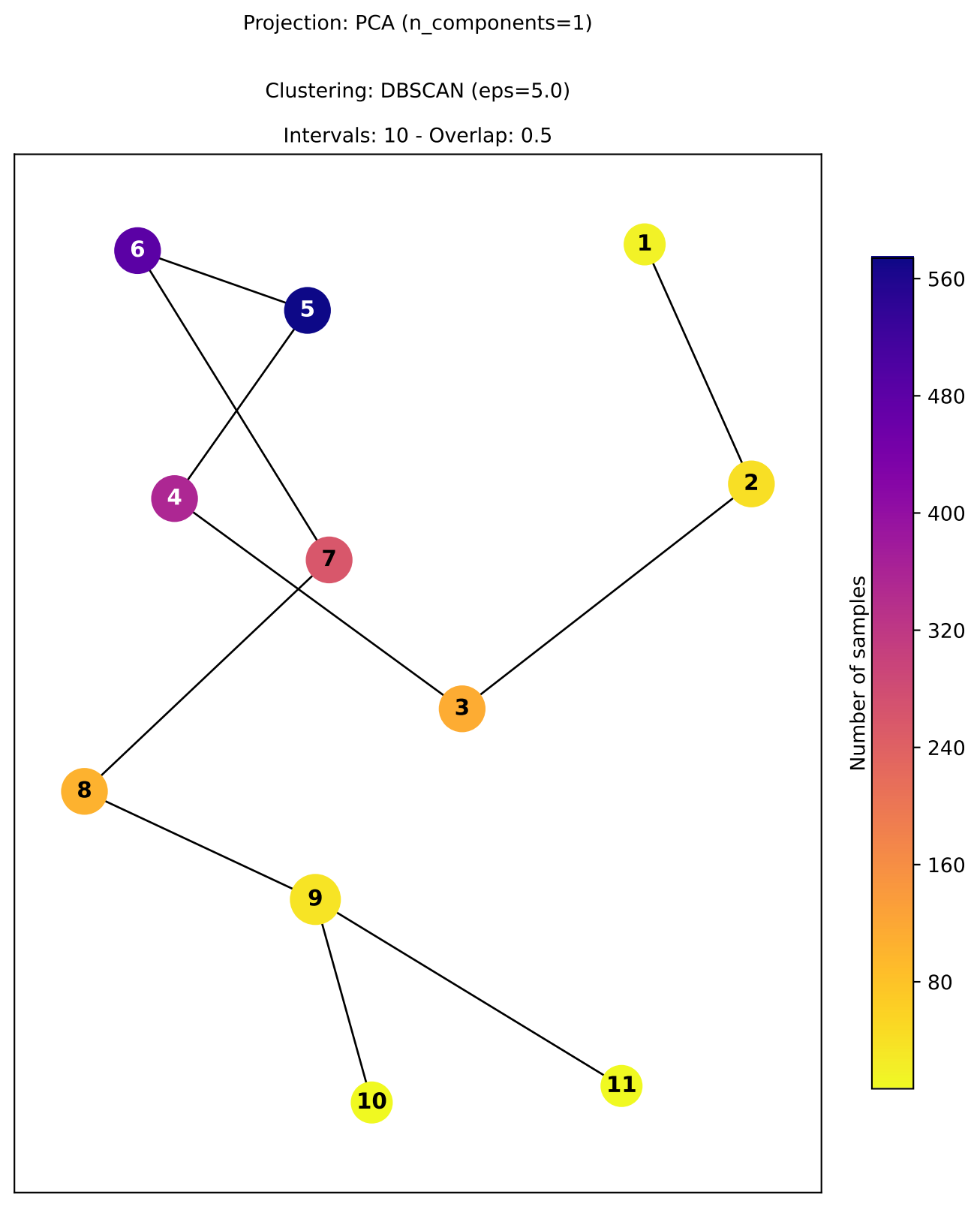
Projection: PCA (n_components=1)
Clustering: DBSCAN (eps=5.0)
Intervals: 10 - Overlap: 0.5
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Number of samples
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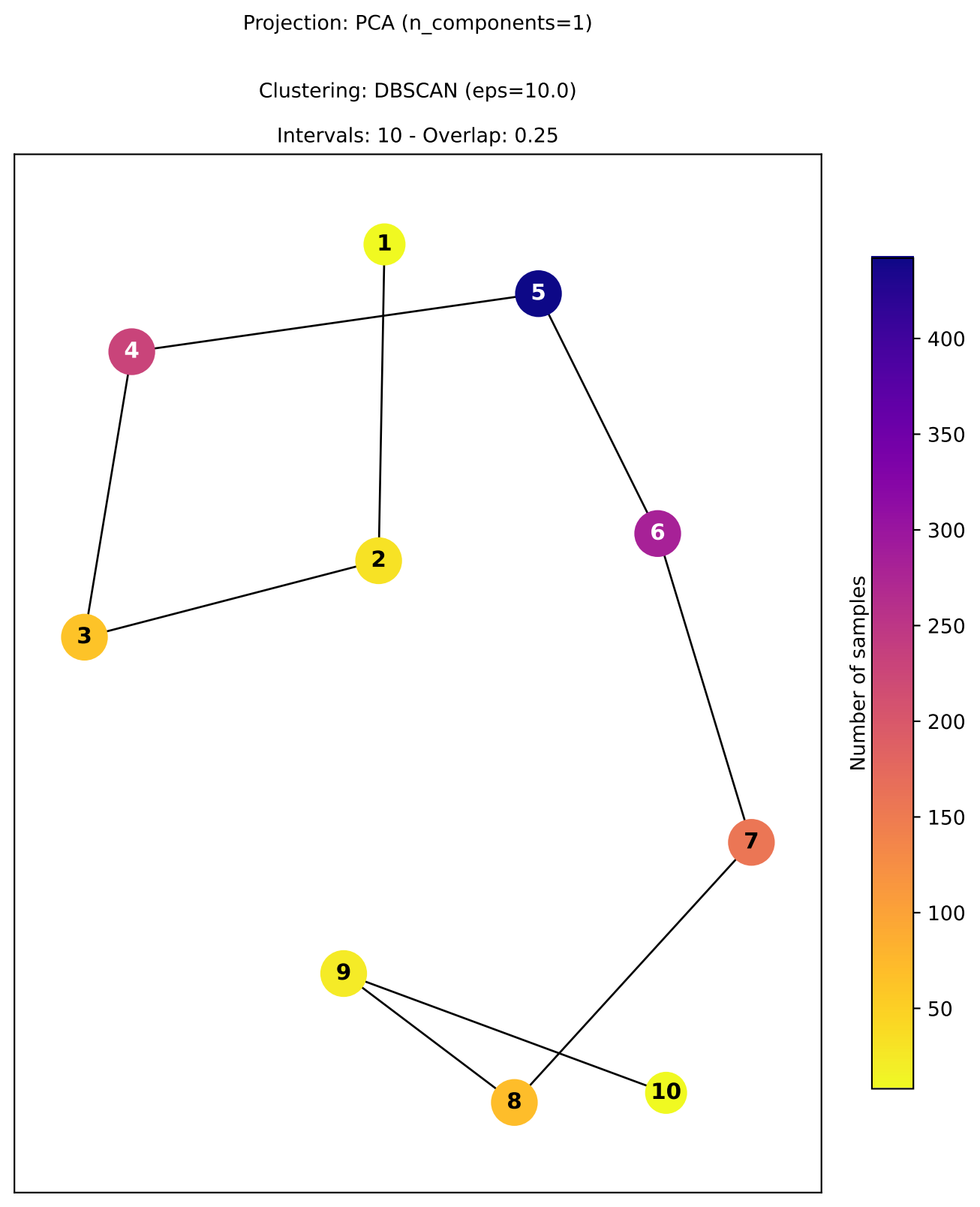
Projection: PCA (n_components=1)
Clustering: DBSCAN (eps=10.0)
Intervals: 10 - Overlap: 0.25
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Number of samples
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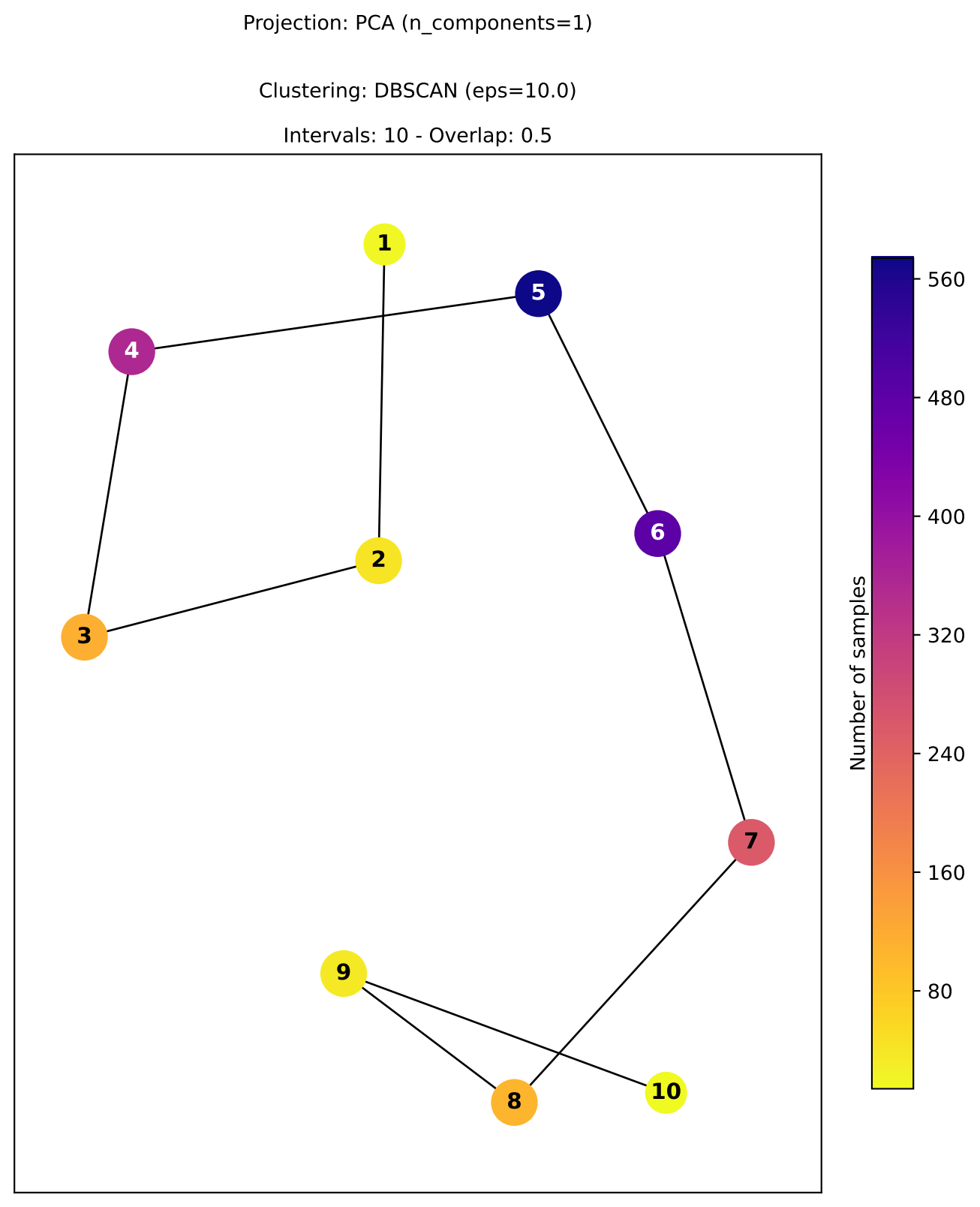
Projection: PCA (n_components=1)
Clustering: DBSCAN (eps=10.0)
Intervals: 10 - Overlap: 0.5
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Number of samples
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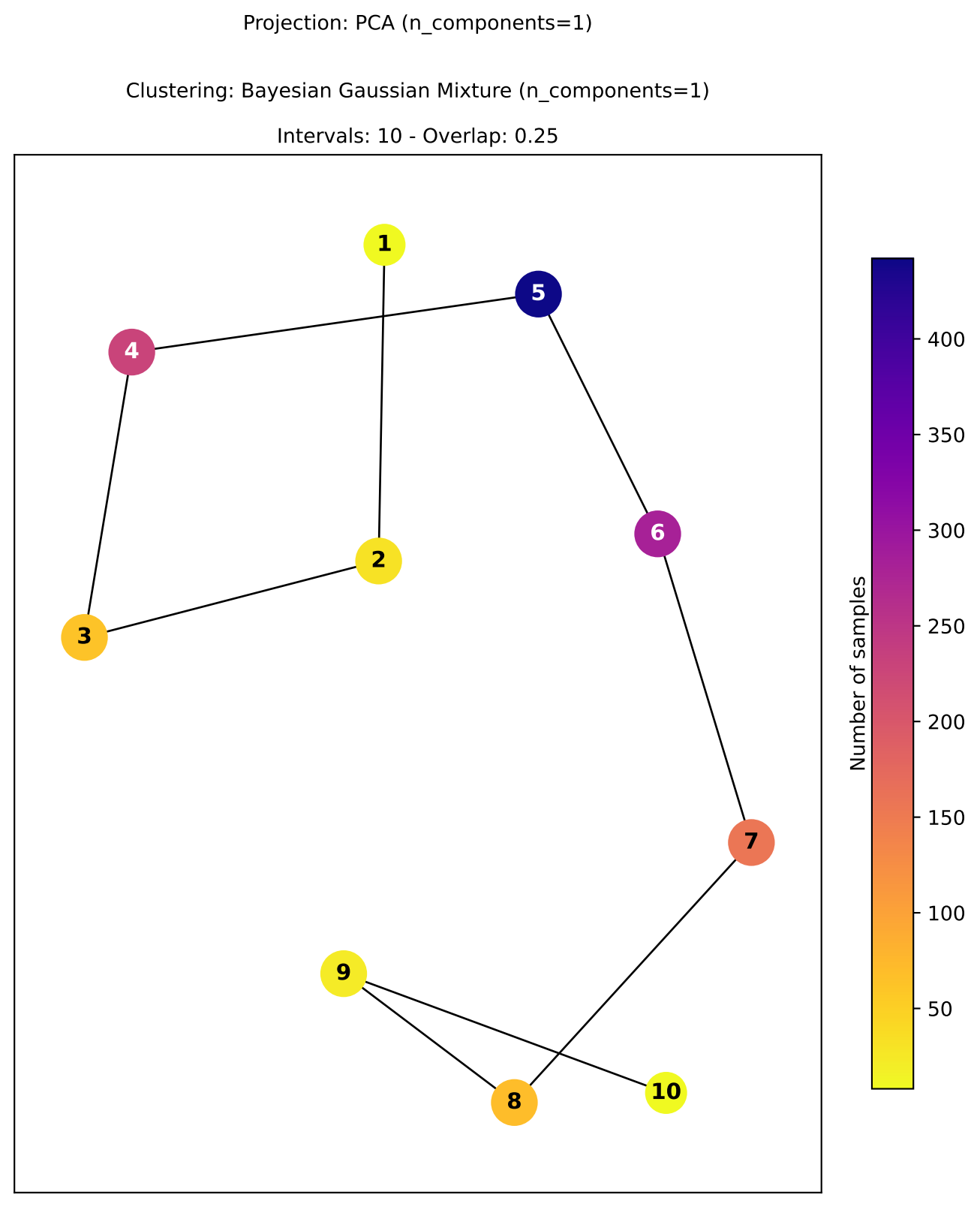
Projection: PCA (n_components=1)
Clustering: Bayesian Gaussian Mixture (n_components=1)
Intervals: 10 - Overlap: 0.25
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Number of samples
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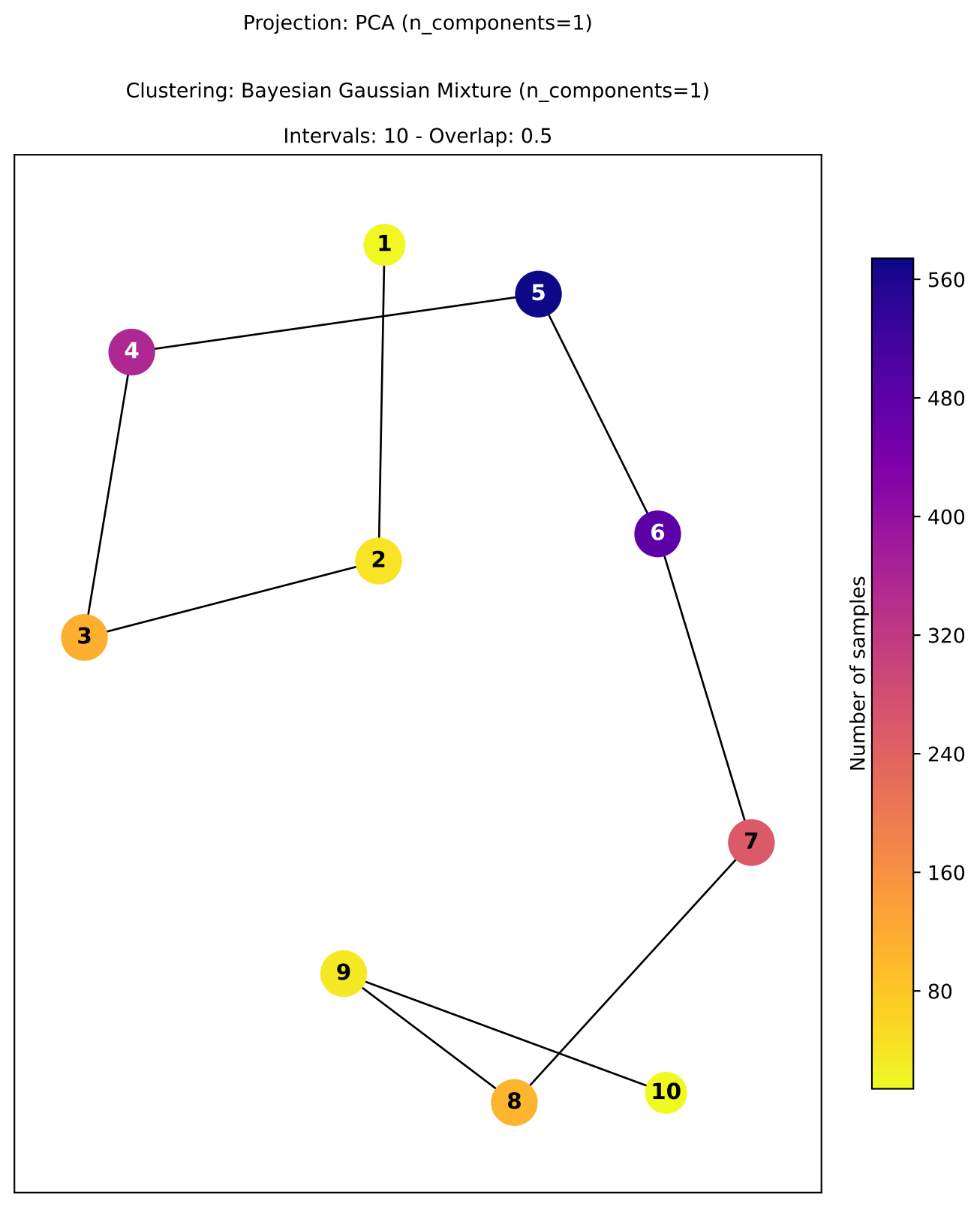
Projection: PCA (n_components=1)
Clustering: Bayesian Gaussian Mixture (n_components=1)
Intervals: 10 - Overlap: 0.5
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Number of samples
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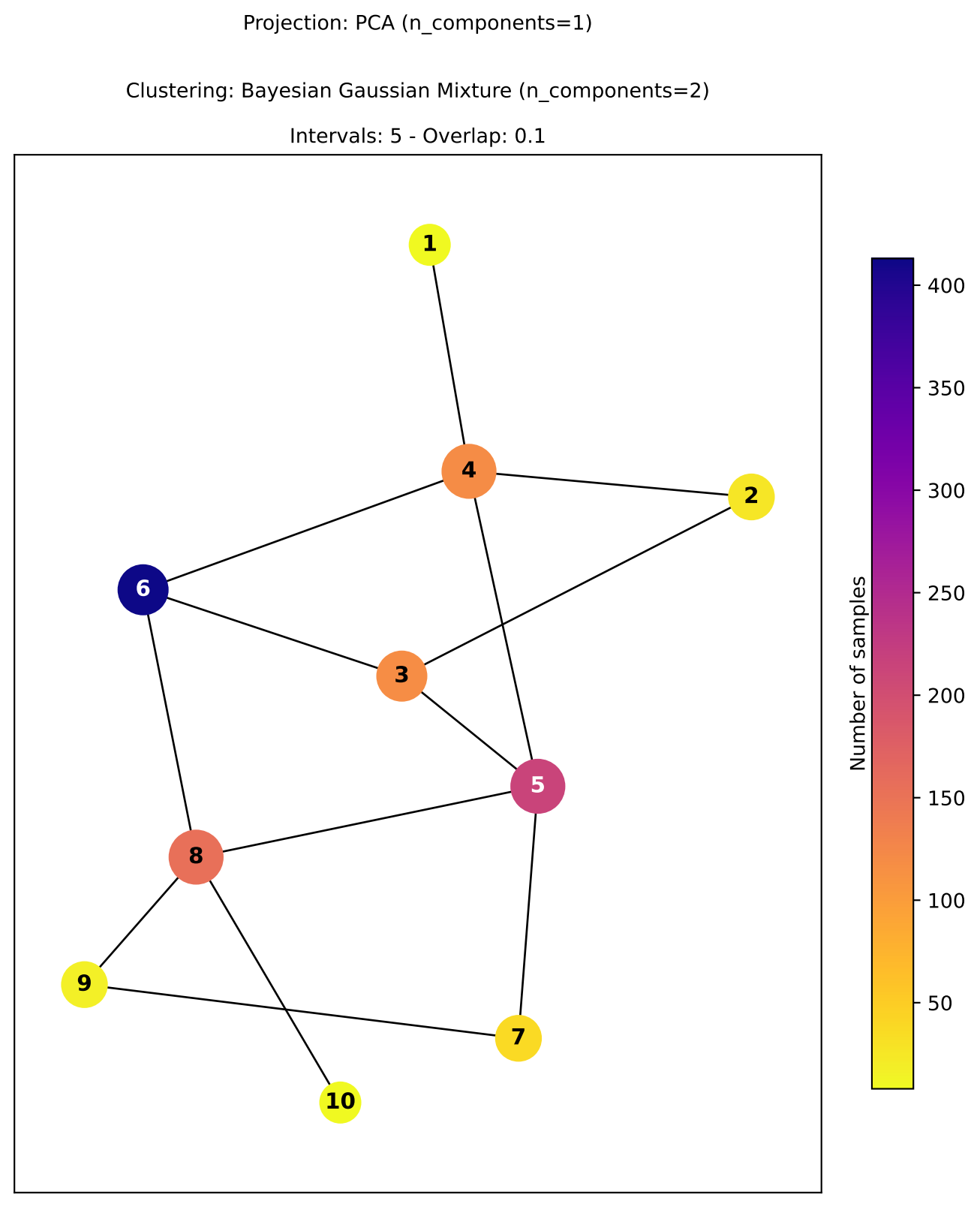
Projection: PCA (n_components=1)
Clustering: Bayesian Gaussian Mixture (n_components=2)
Intervals: 5 - Overlap: 0.1
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Number of samples
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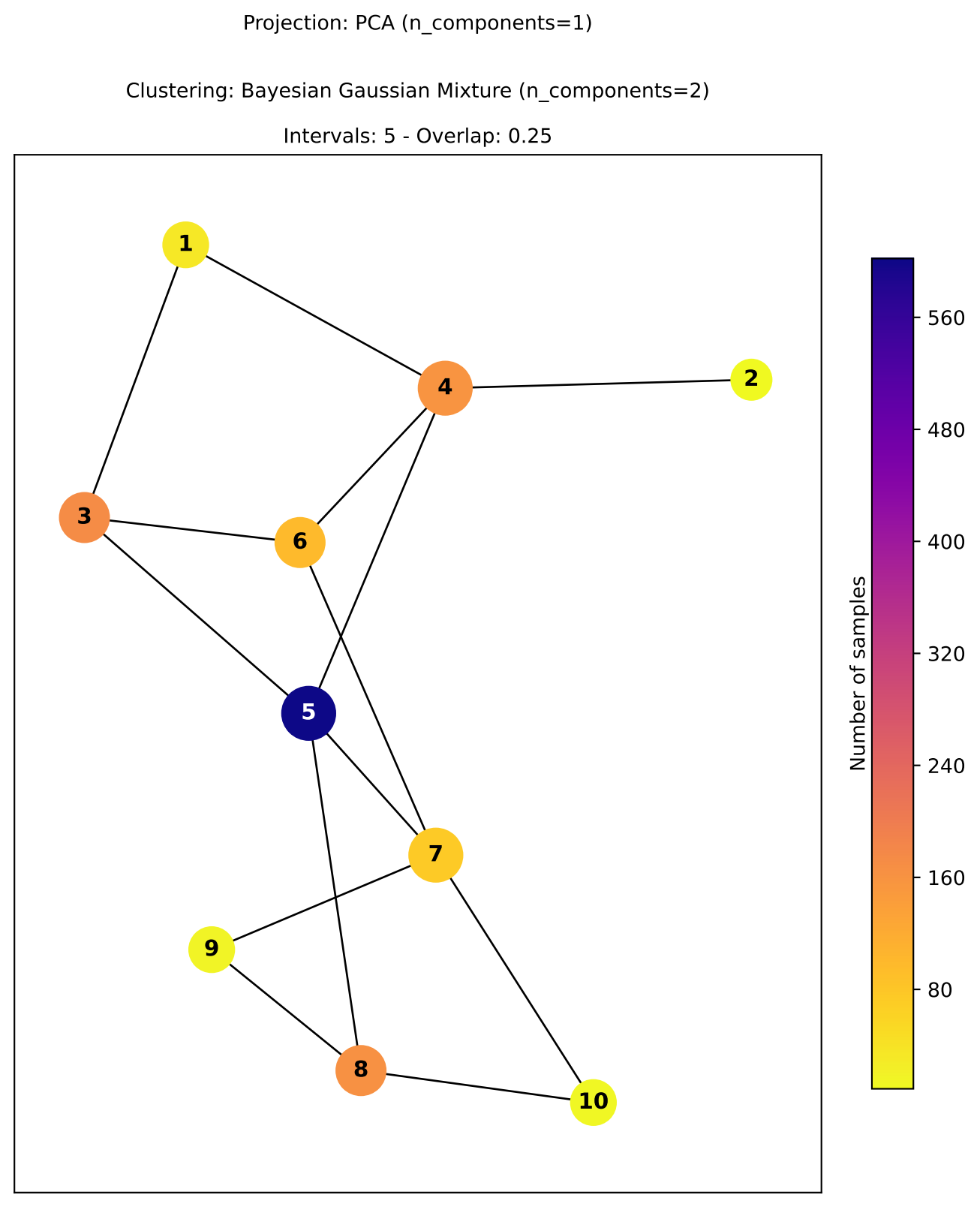
Projection: PCA (n_components=1)
Clustering: Bayesian Gaussian Mixture (n_components=2)
Intervals: 5 - Overlap: 0.25
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Number of samples
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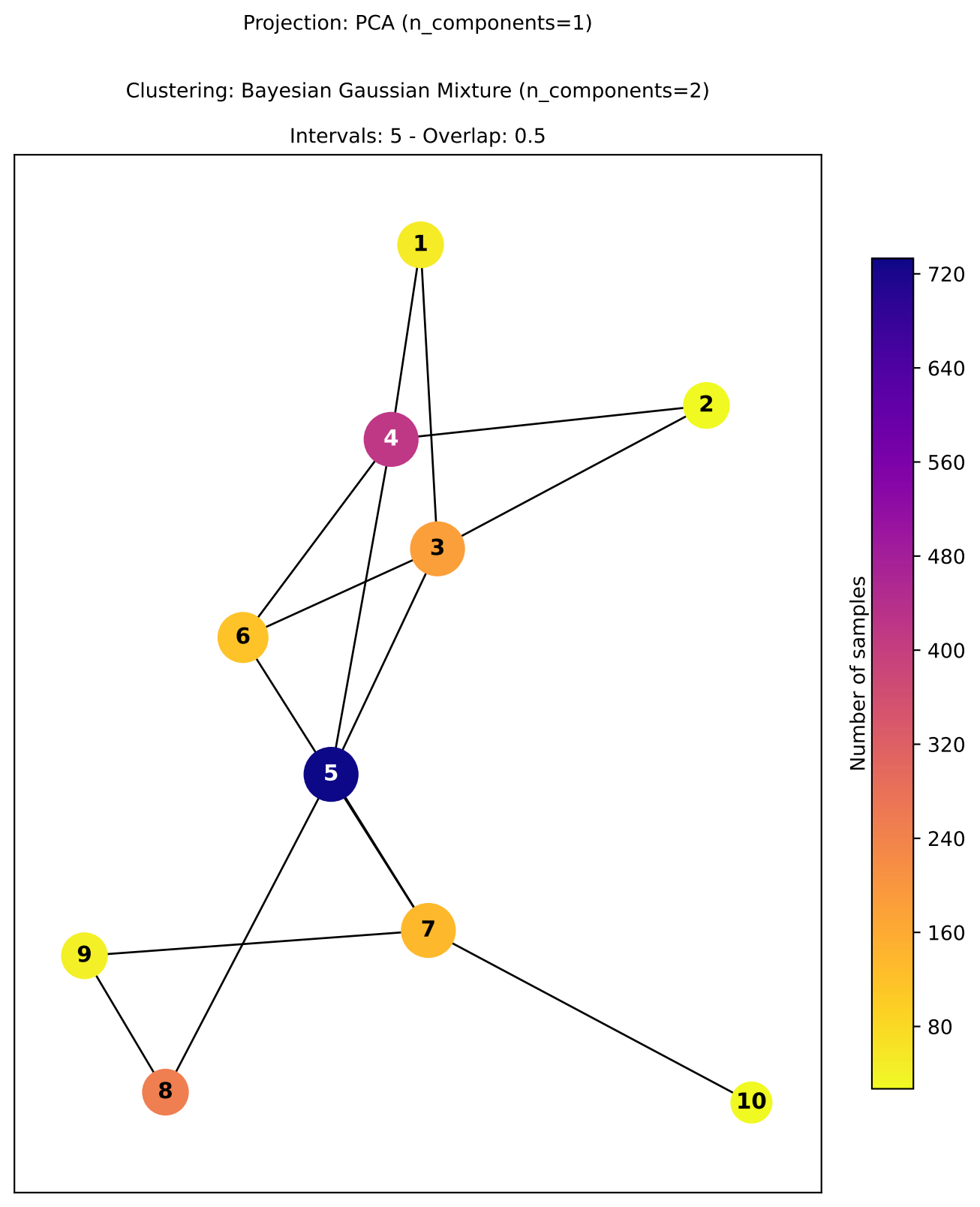
Projection: PCA (n_components=1)
Clustering: Bayesian Gaussian Mixture (n_components=2)
Intervals: 5 - Overlap: 0.5
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Number of samples
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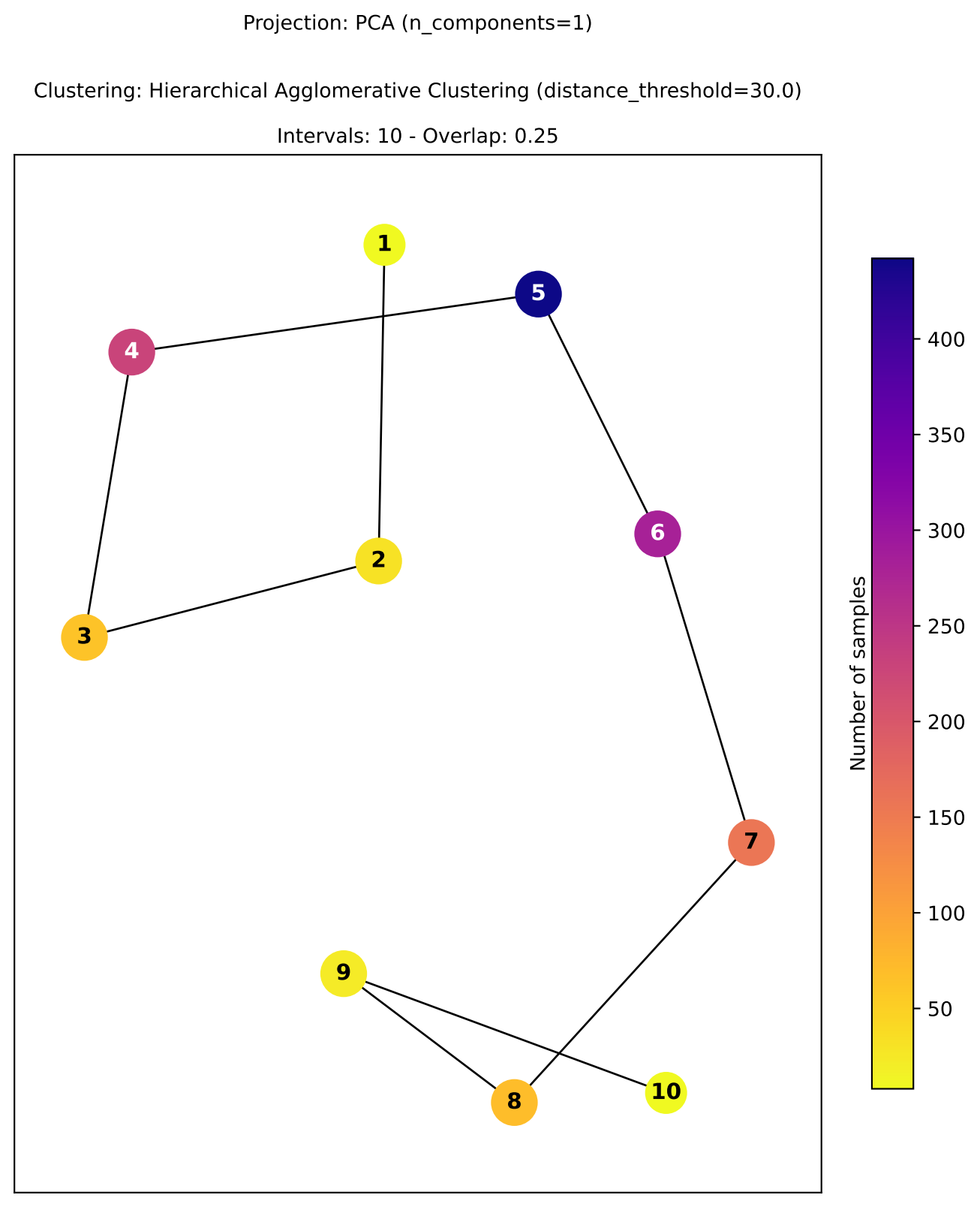
Projection: PCA (n_components=1)
Clustering: Hierarchical Agglomerative Clustering (distance_threshold=30.0)
Intervals: 10 - Overlap: 0.25
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Number of samples
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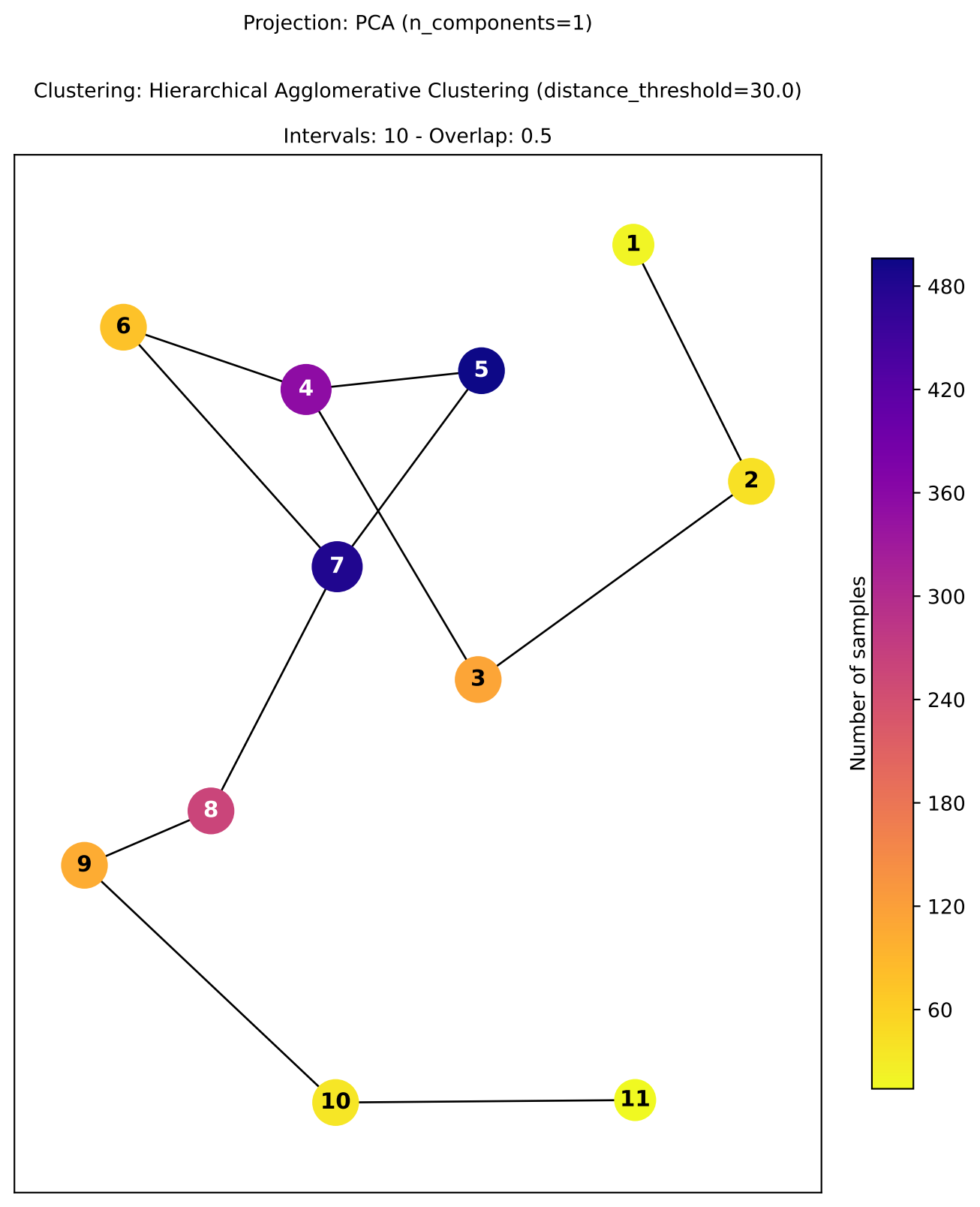
Projection: PCA (n_components=1)
Clustering: Hierarchical Agglomerative Clustering (distance_threshold=30.0)
Intervals: 10 - Overlap: 0.5
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Number of samples
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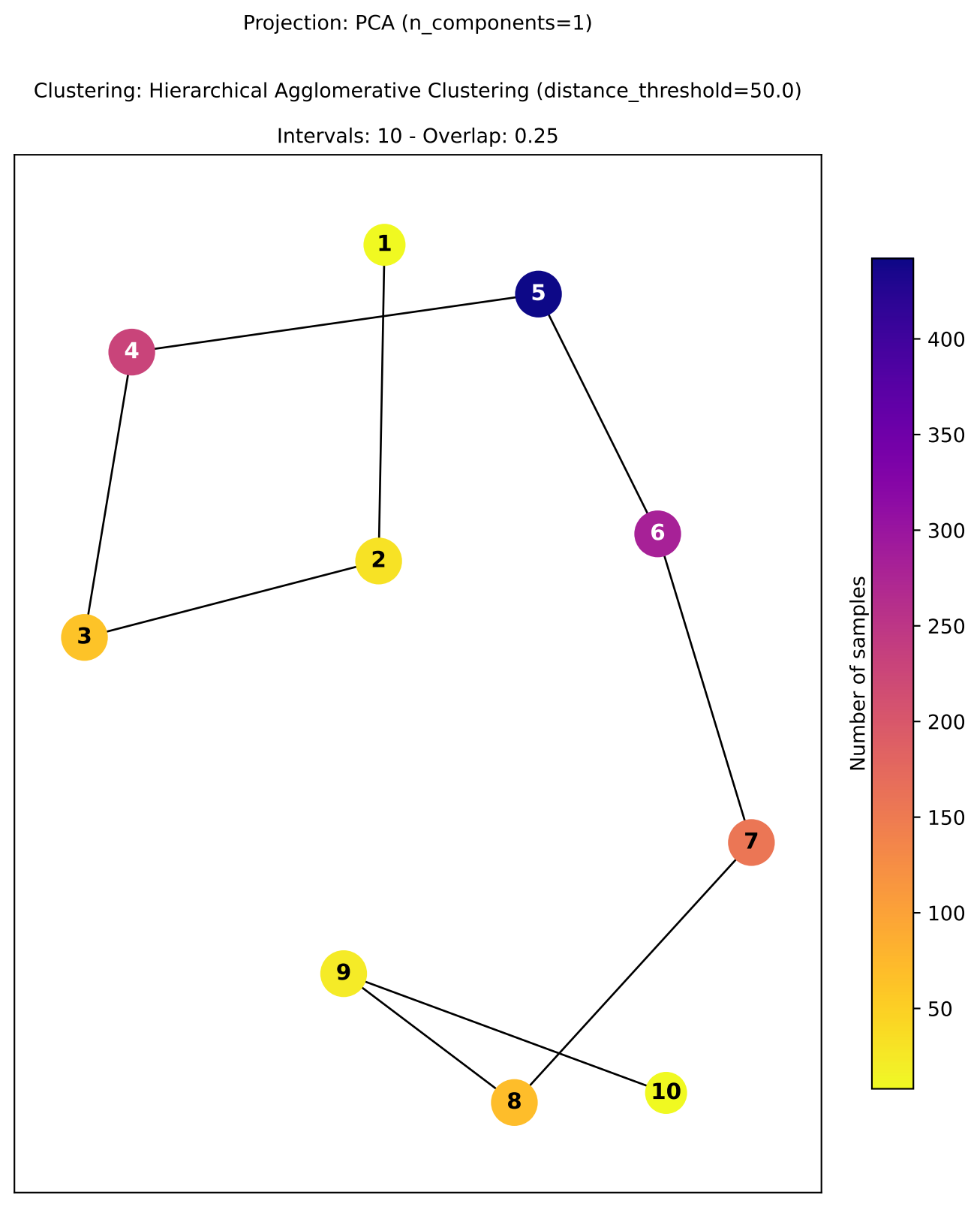
Projection: PCA (n_components=1)
Clustering: Hierarchical Agglomerative Clustering (distance_threshold=50.0)
Intervals: 10 - Overlap: 0.25
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Number of samples
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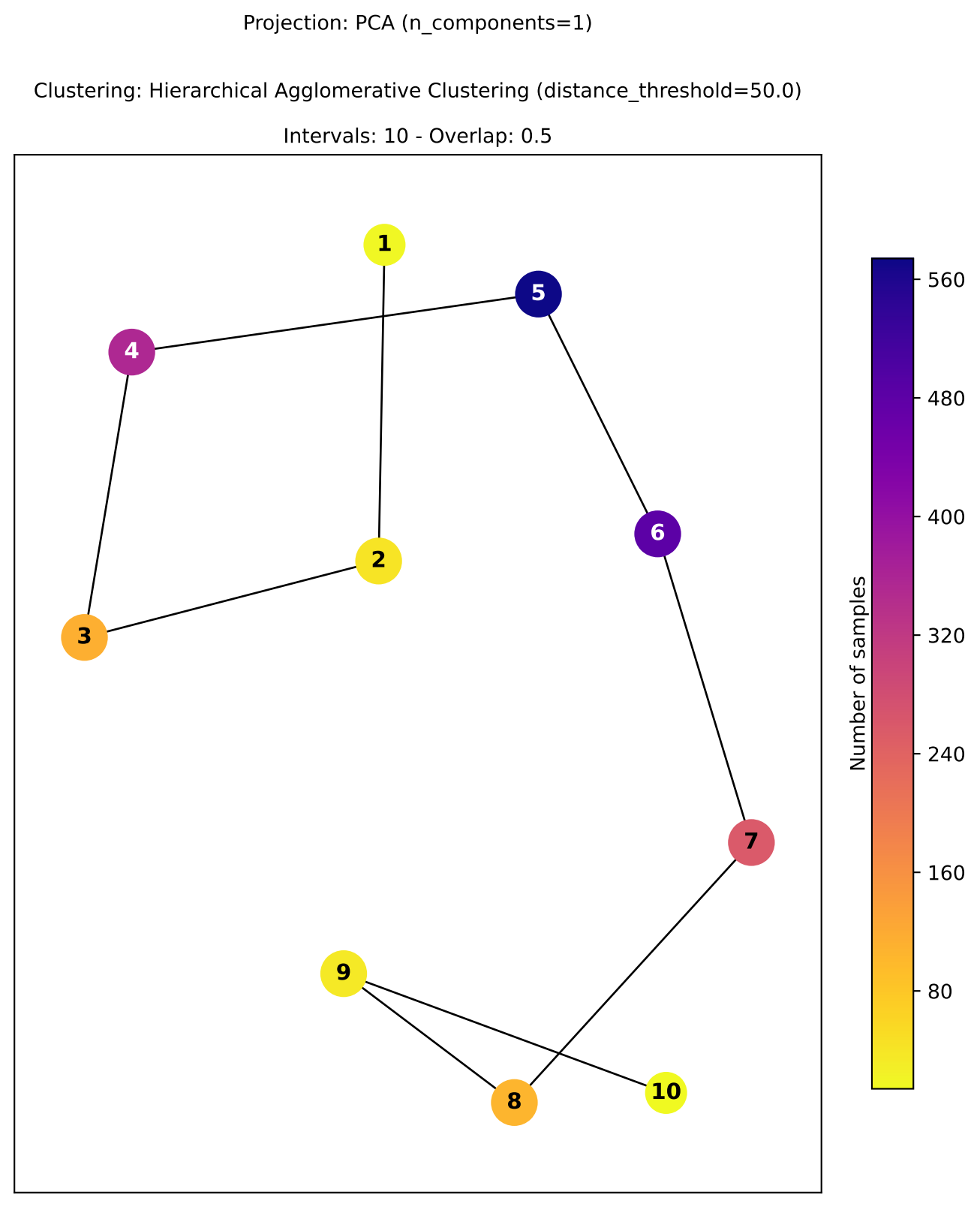
Projection: PCA (n_components=1)
Clustering: Hierarchical Agglomerative Clustering (distance_threshold=50.0)
Intervals: 10 - Overlap: 0.5
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Number of samples
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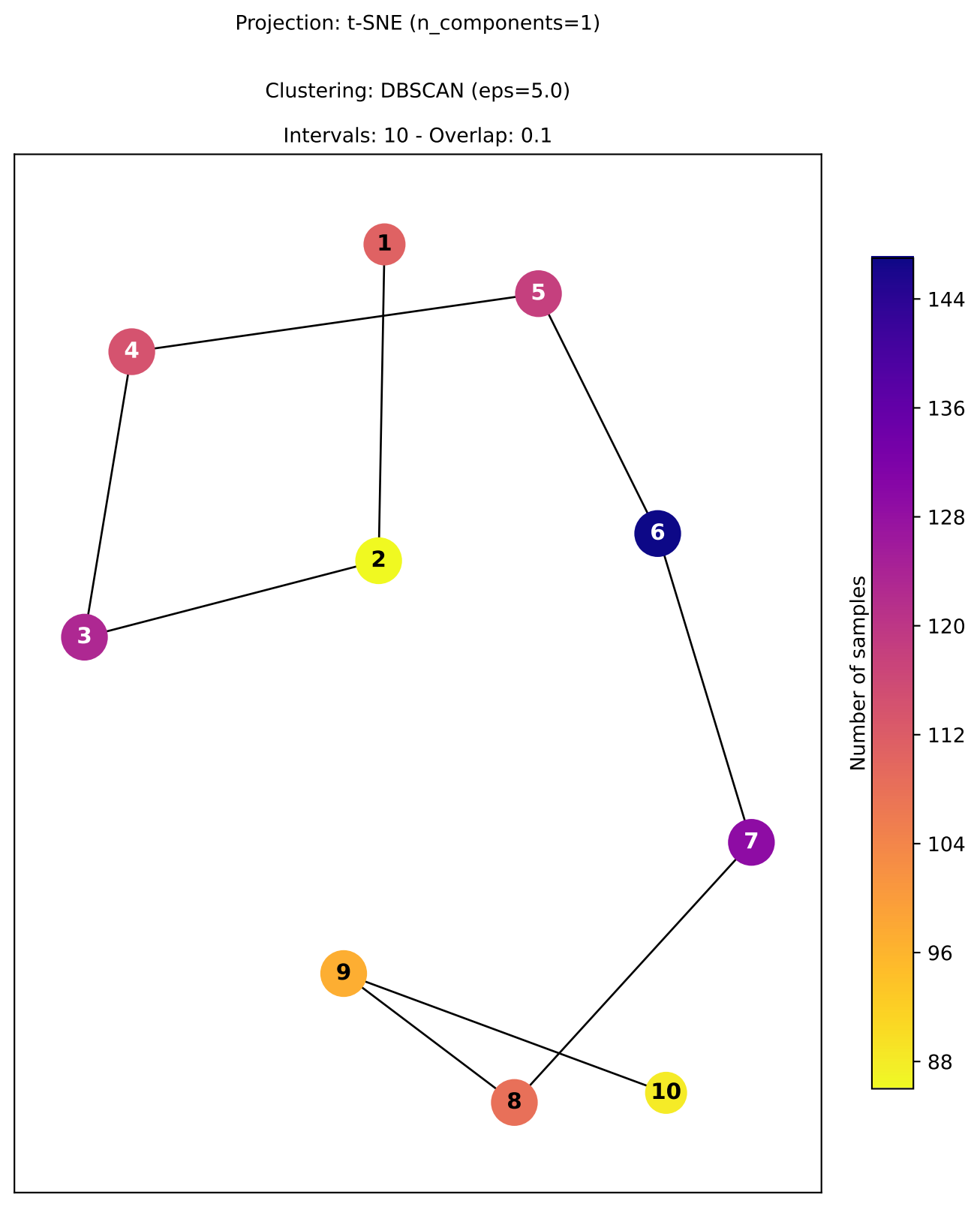
Projection: t-SNE (n_components=1)
Clustering: DBSCAN (eps=5.0)
Intervals: 10 - Overlap: 0.1
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Number of samples
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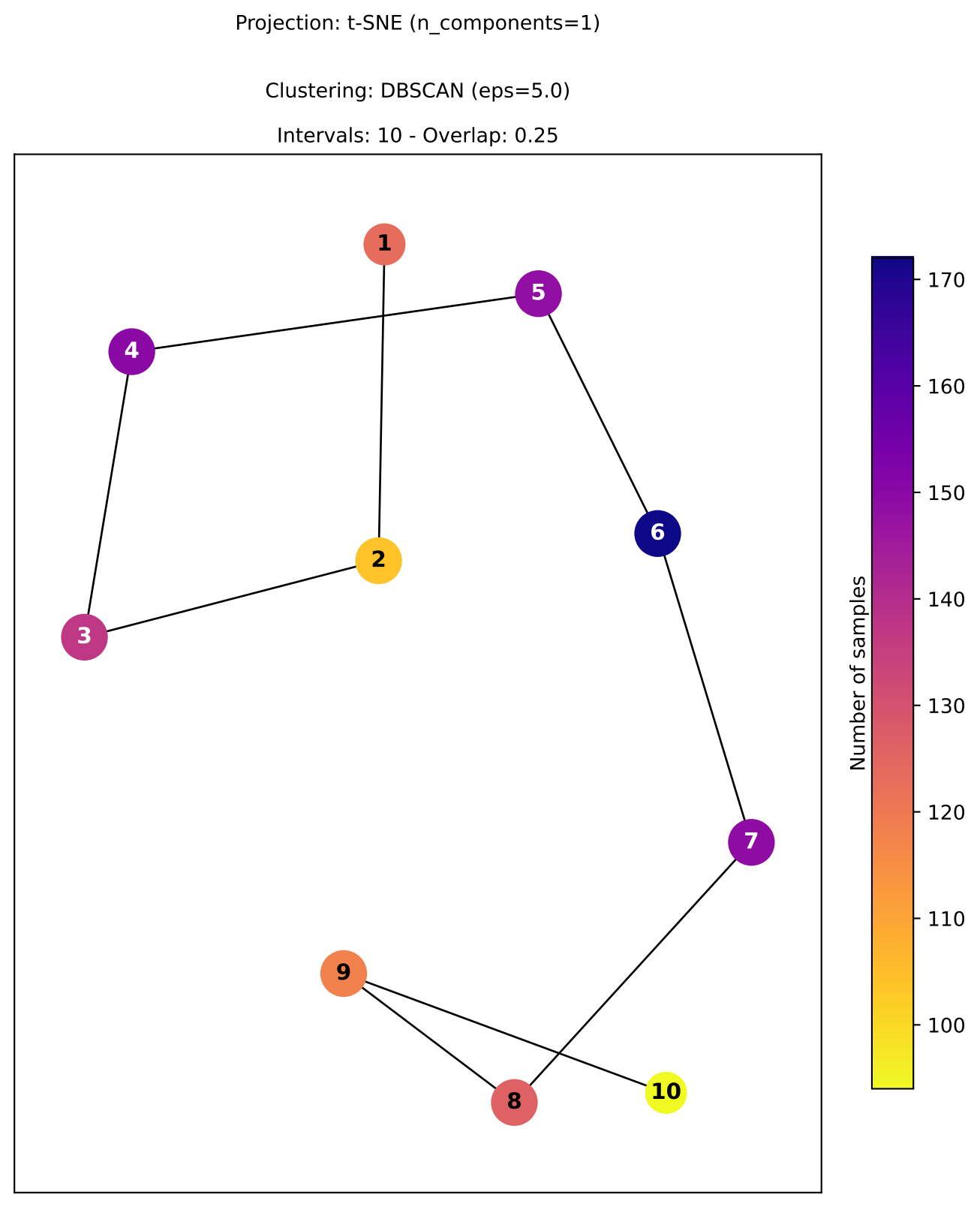
Projection: t-SNE (n_components=1)
Clustering: DBSCAN (eps=5.0)
Intervals: 10 - Overlap: 0.25
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Number of samples
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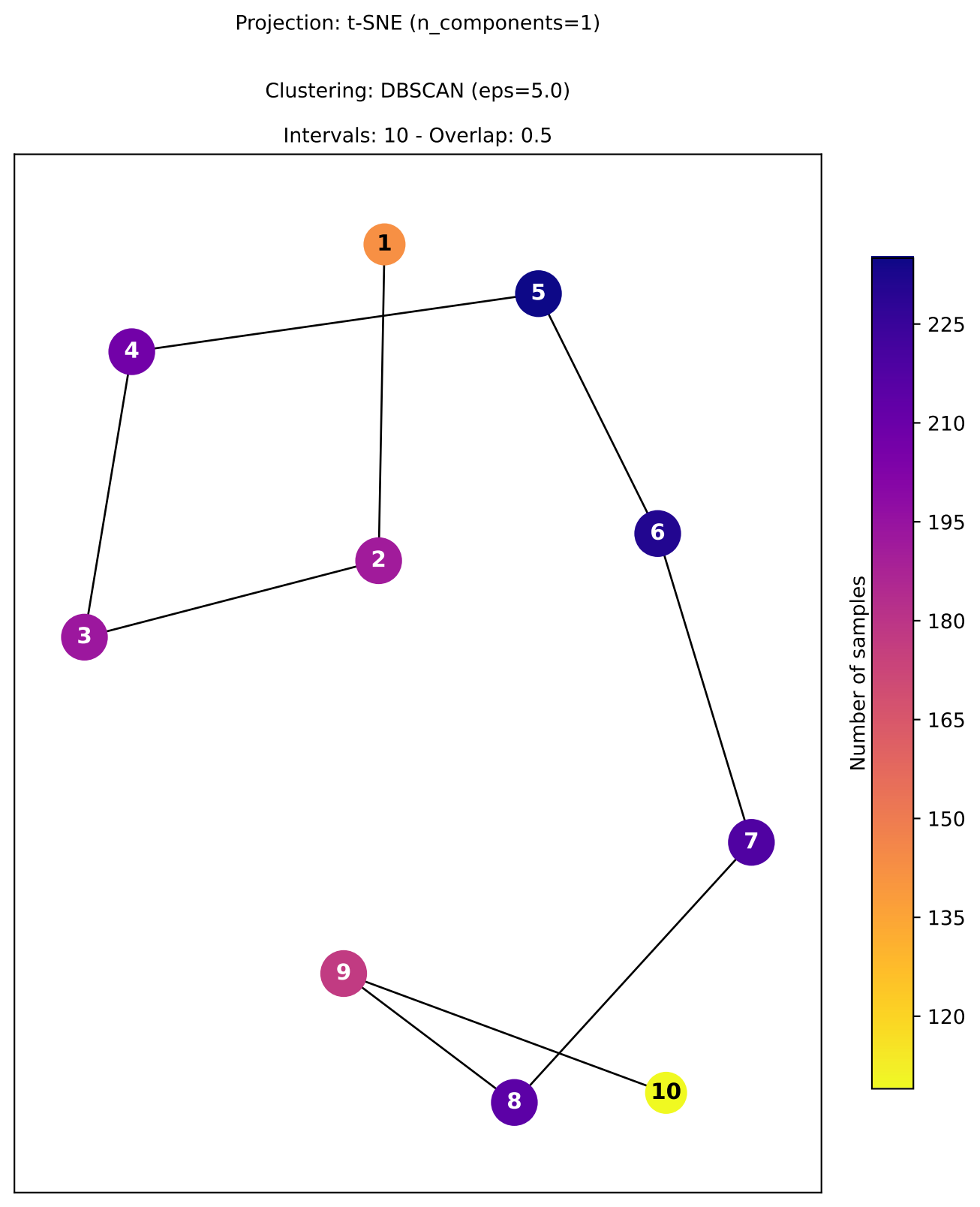
Projection: t-SNE (n_components=1)
Clustering: DBSCAN (eps=5.0)
Intervals: 10 - Overlap: 0.5
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Number of samples
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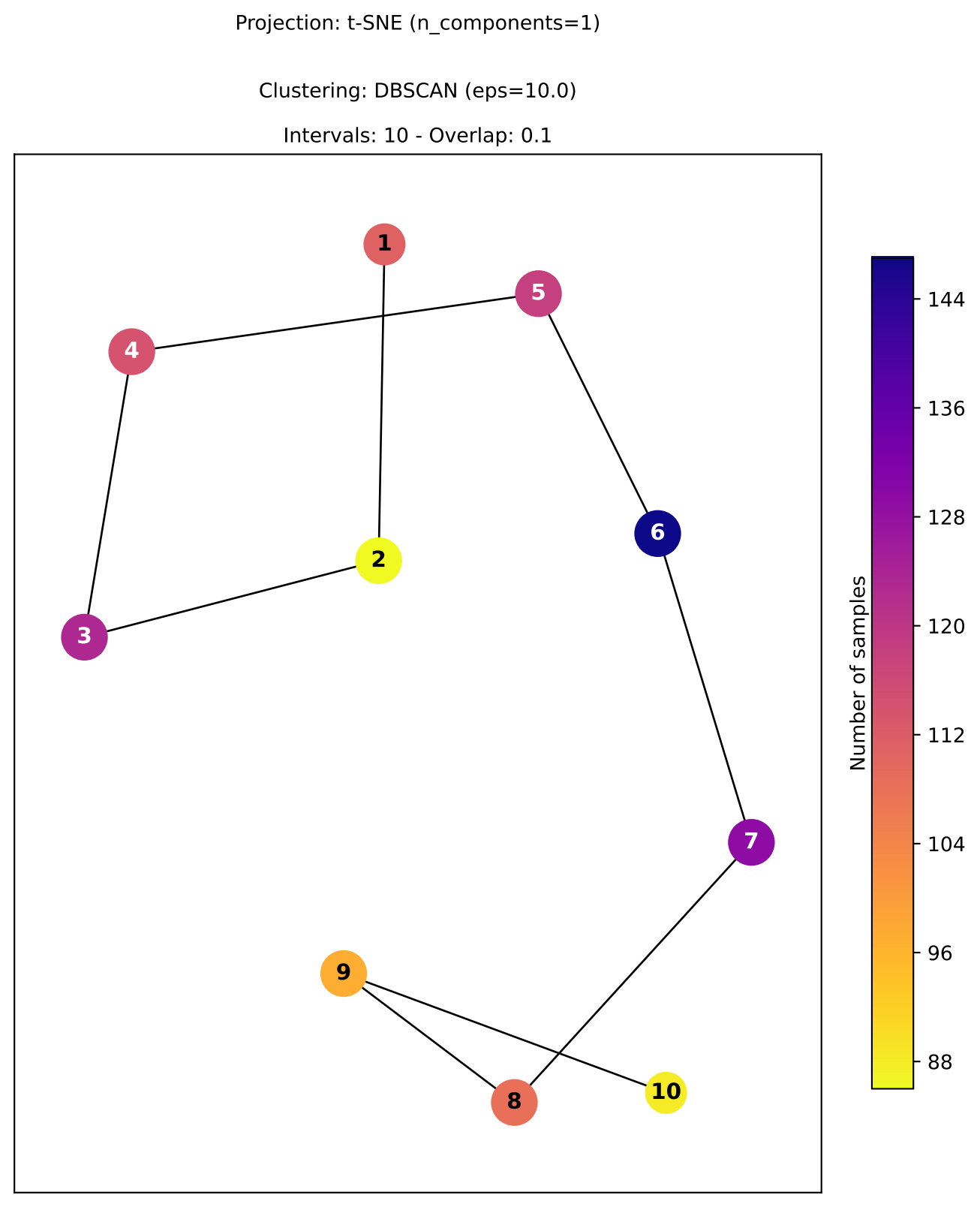
Projection: t-SNE (n_components=1)
Clustering: DBSCAN (eps=10.0)
Intervals: 10 - Overlap: 0.1
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Number of samples
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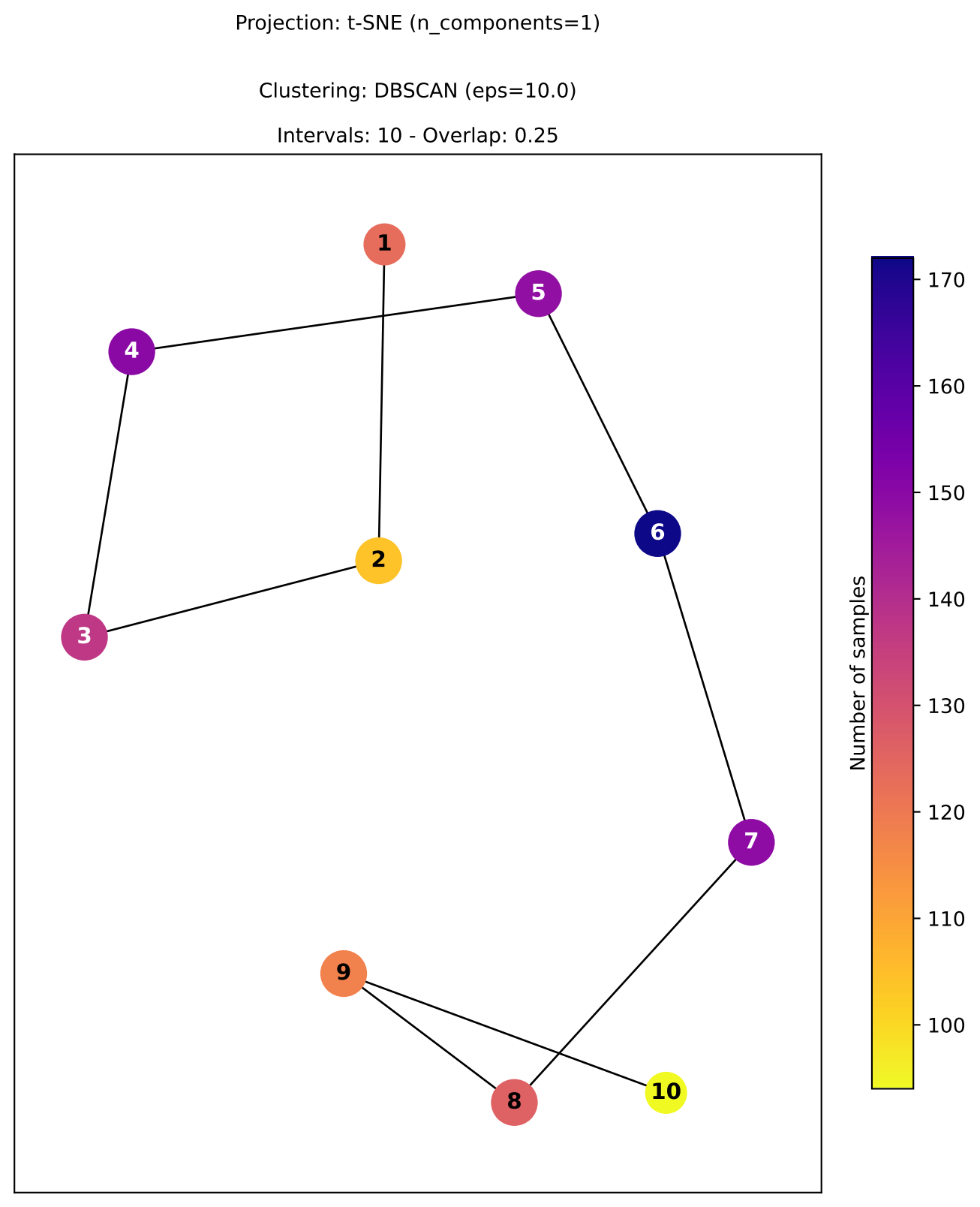
Projection: t-SNE (n_components=1)
Clustering: DBSCAN (eps=10.0)
Intervals: 10 - Overlap: 0.25
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Number of samples
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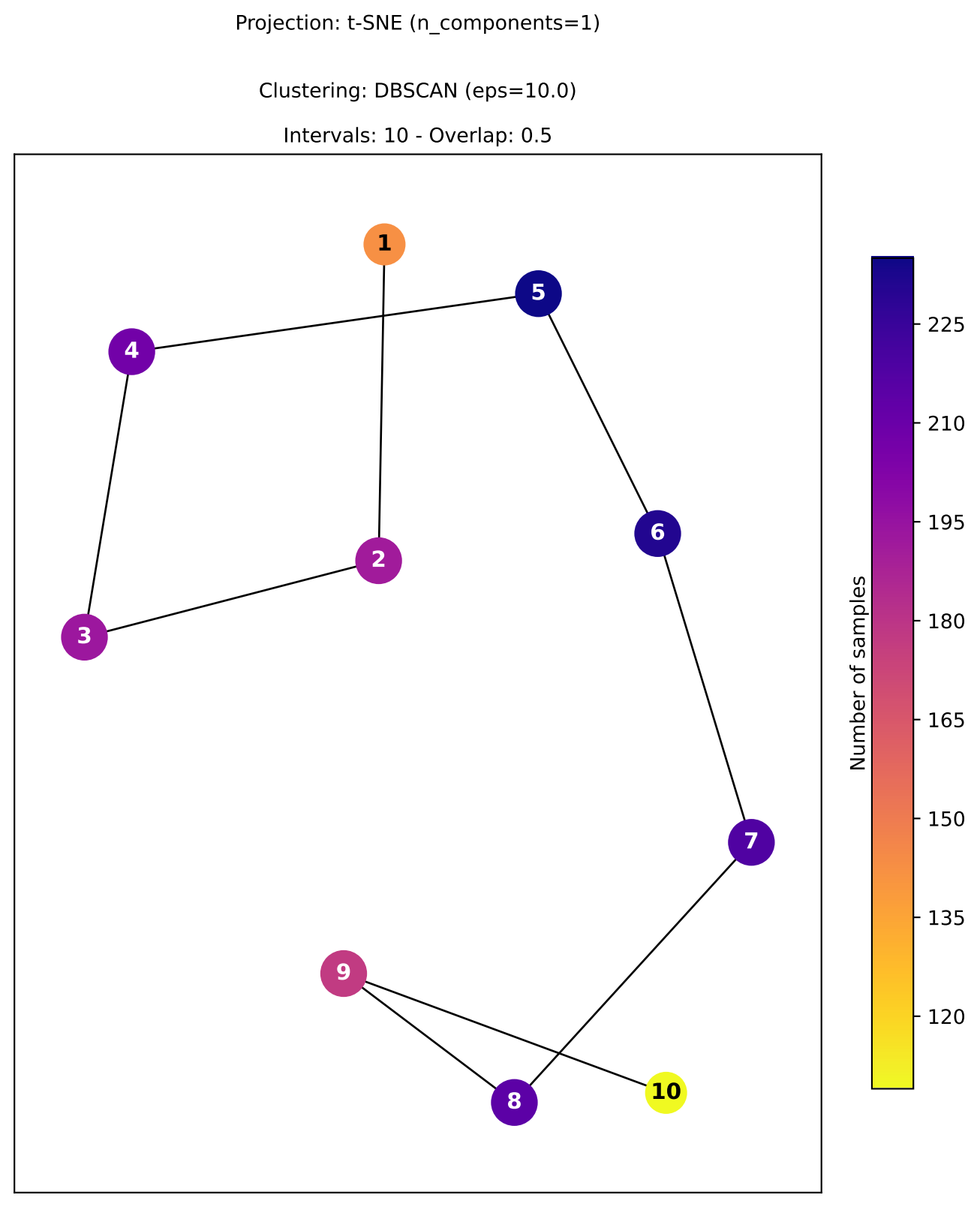
Projection: t-SNE (n_components=1)
Clustering: DBSCAN (eps=10.0)
Intervals: 10 - Overlap: 0.5
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Number of samples
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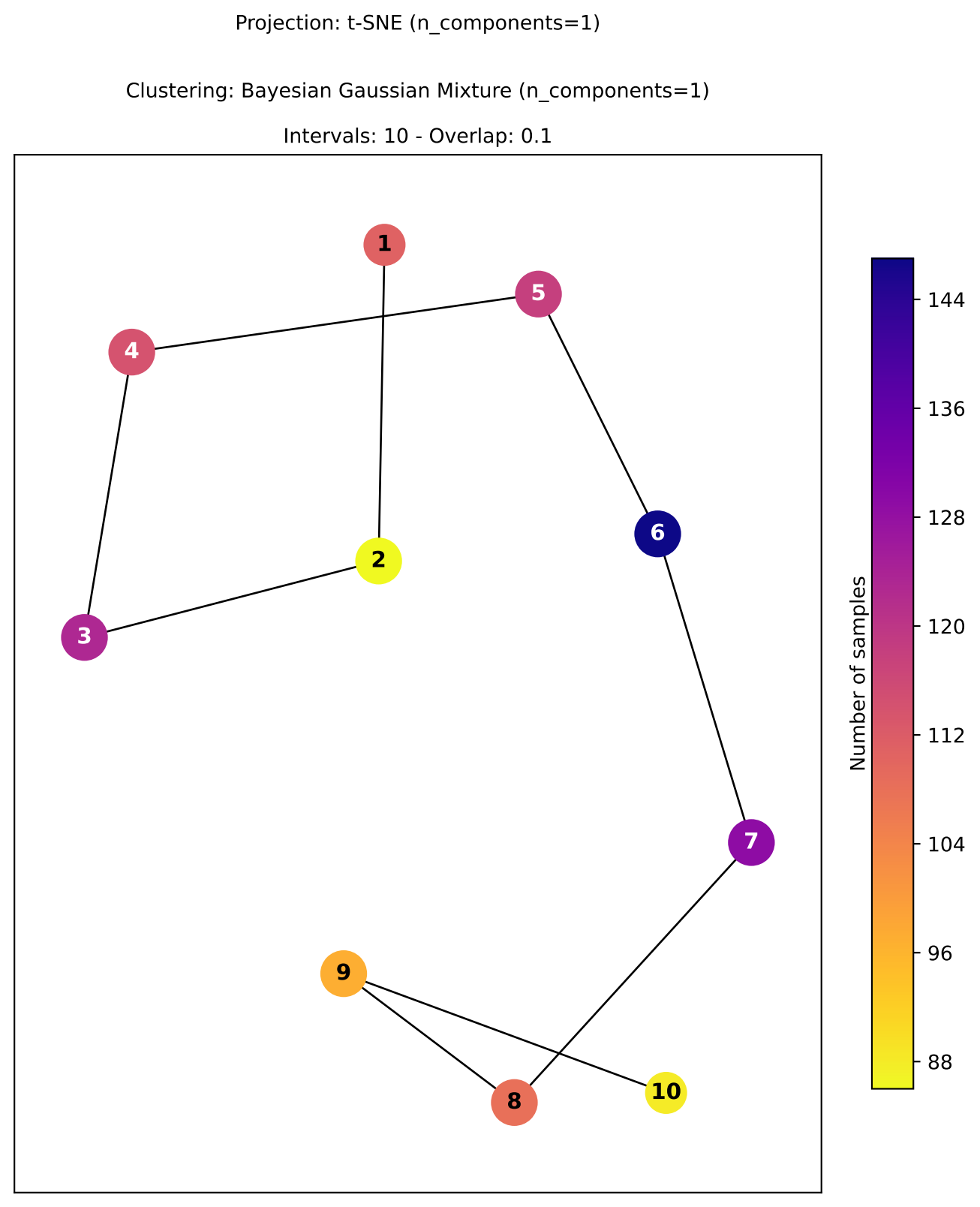
Projection: t-SNE (n_components=1)
Clustering: Bayesian Gaussian Mixture (n_components=1)
Intervals: 10 - Overlap: 0.1
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Number of samples
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128
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112
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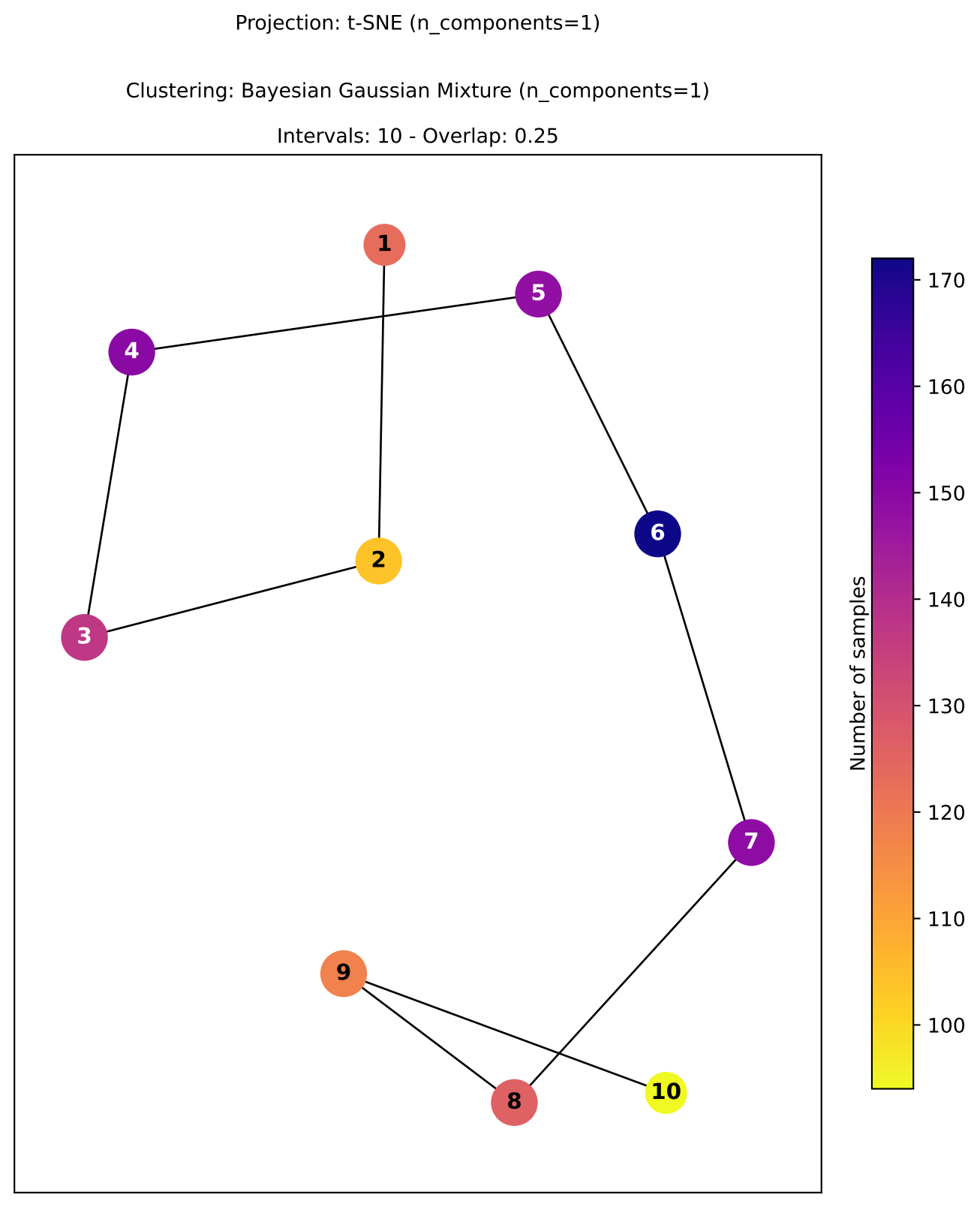
Projection: t-SNE (n_components=1)
Clustering: Bayesian Gaussian Mixture (n_components=1)
Intervals: 10 - Overlap: 0.25
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Number of samples
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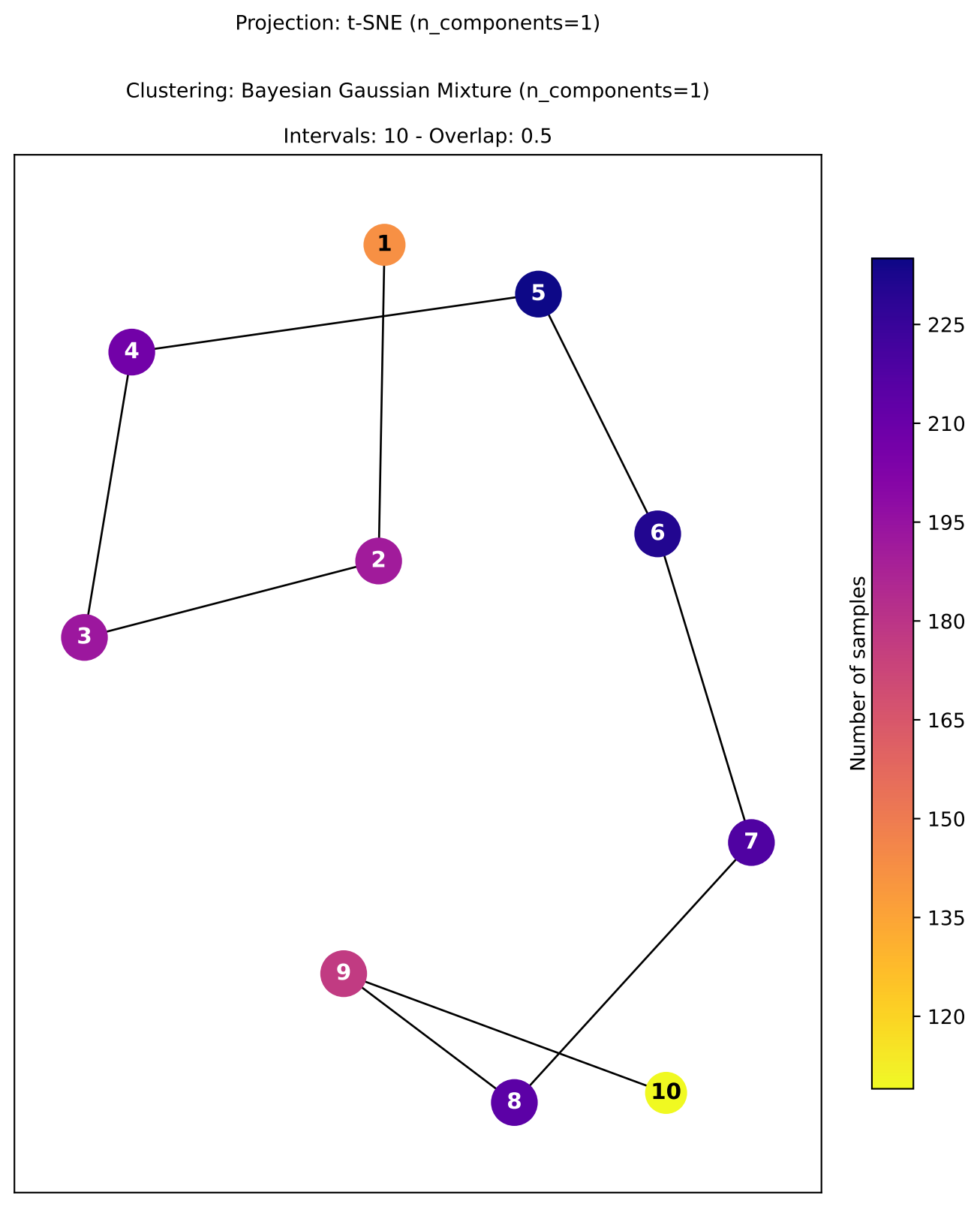
100


Projection: t-SNE (n_components=1)
Clustering: Bayesian Gaussian Mixture (n_components=1)
Intervals: 10 - Overlap: 0.5
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Number of samples
225
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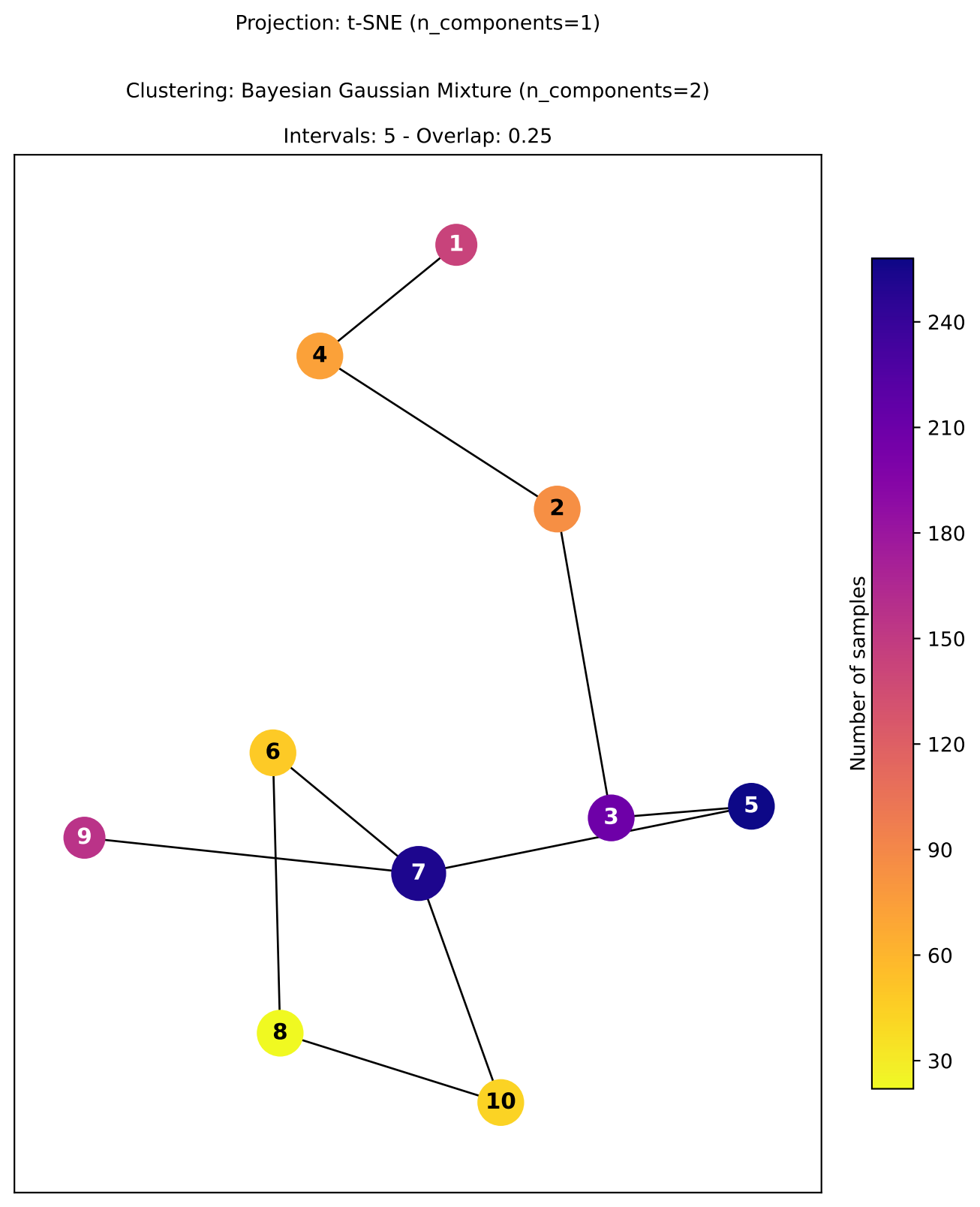
Projection: t-SNE (n_components=1)
Clustering: Bayesian Gaussian Mixture (n_components=2)
Intervals: 5 - Overlap: 0.25
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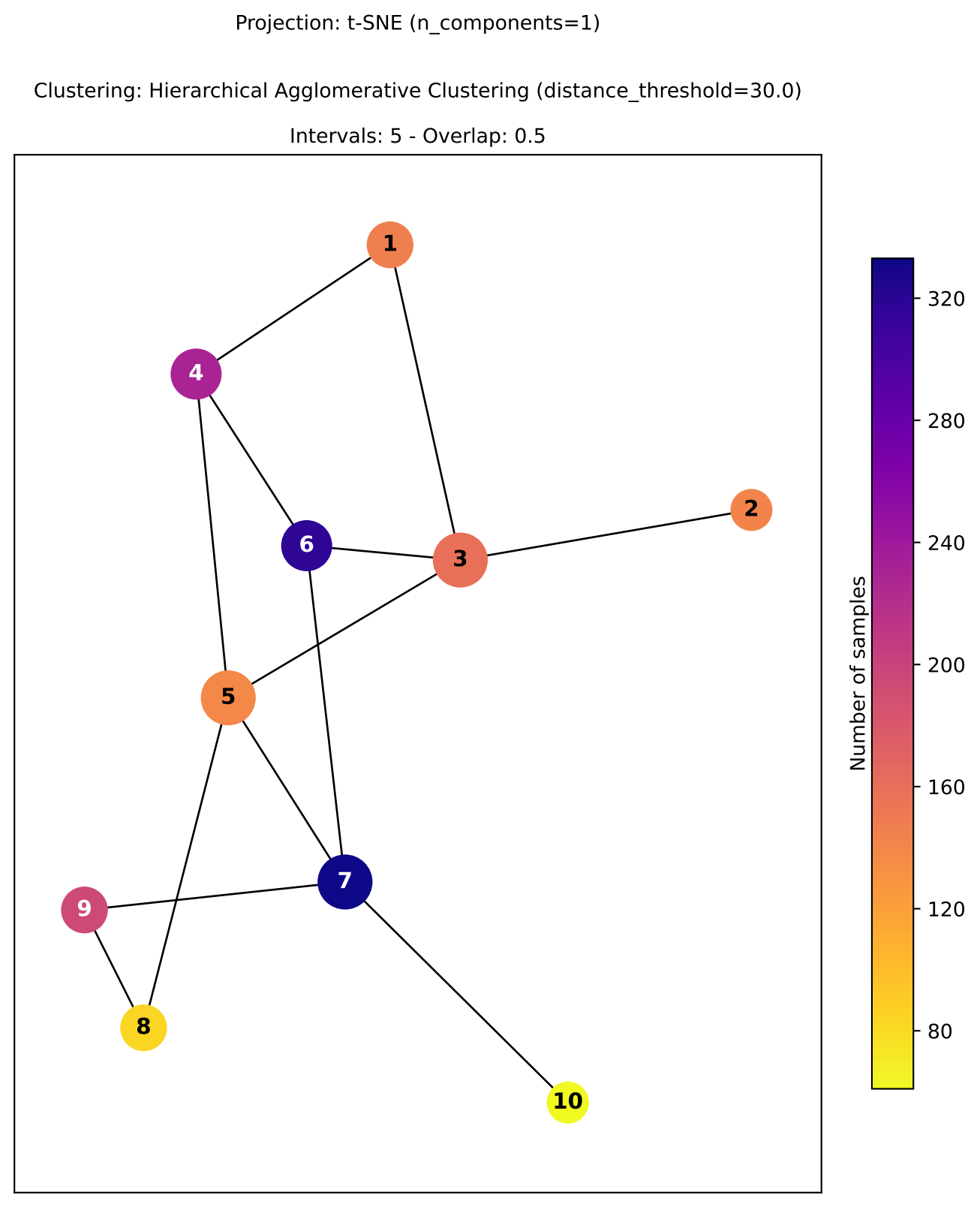
10
Number of samples
240
210
180
150
120
90
60
30


Projection: t-SNE (n_components=1)
Clustering: Hierarchical Agglomerative Clustering (distance_threshold=30.0)
Intervals: 5 - Overlap: 0.5
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Number of samples
320
280
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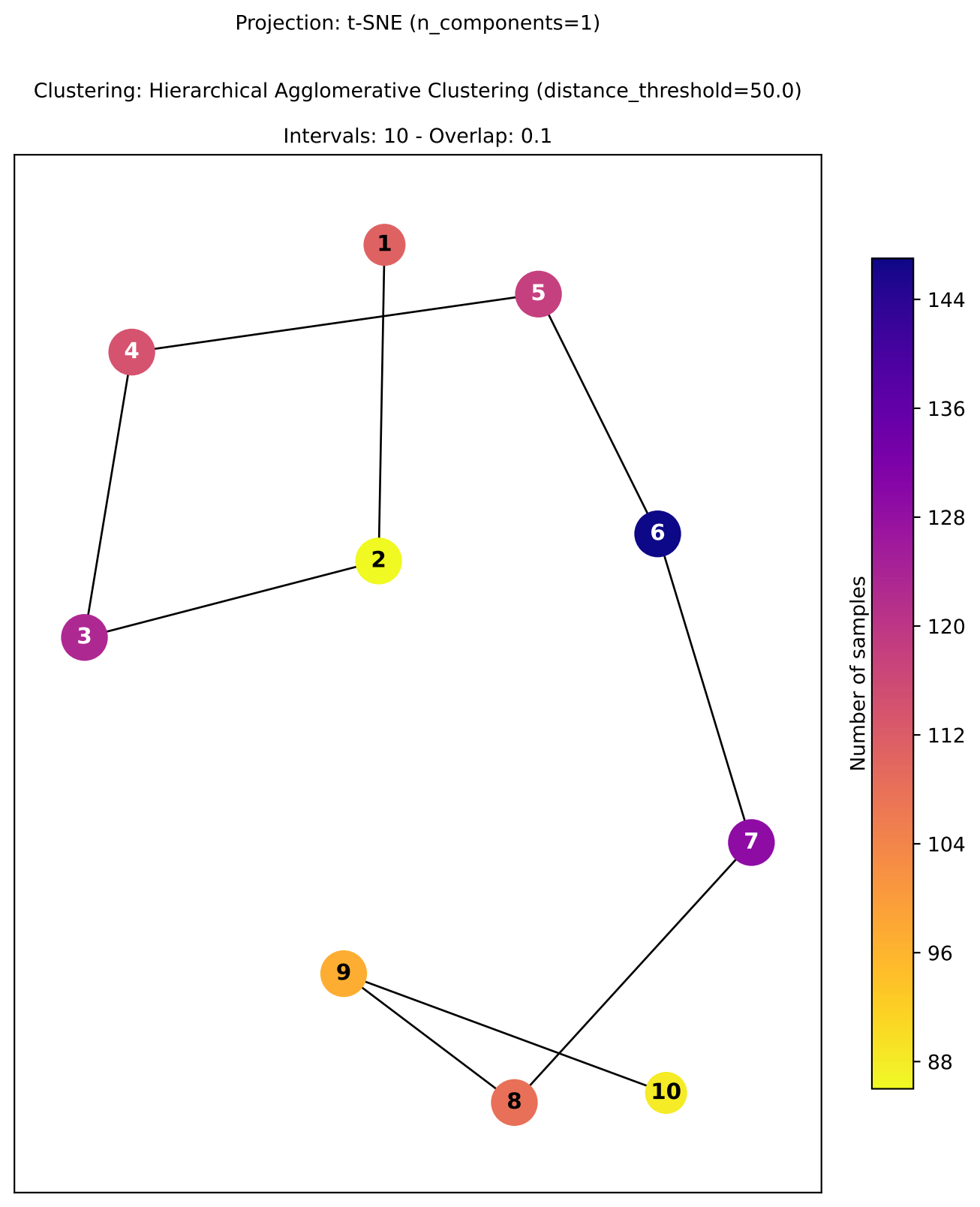
Projection: t-SNE (n_components=1)
Clustering: Hierarchical Agglomerative Clustering (distance_threshold=50.0)
Intervals: 10 - Overlap: 0.1
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Number of samples
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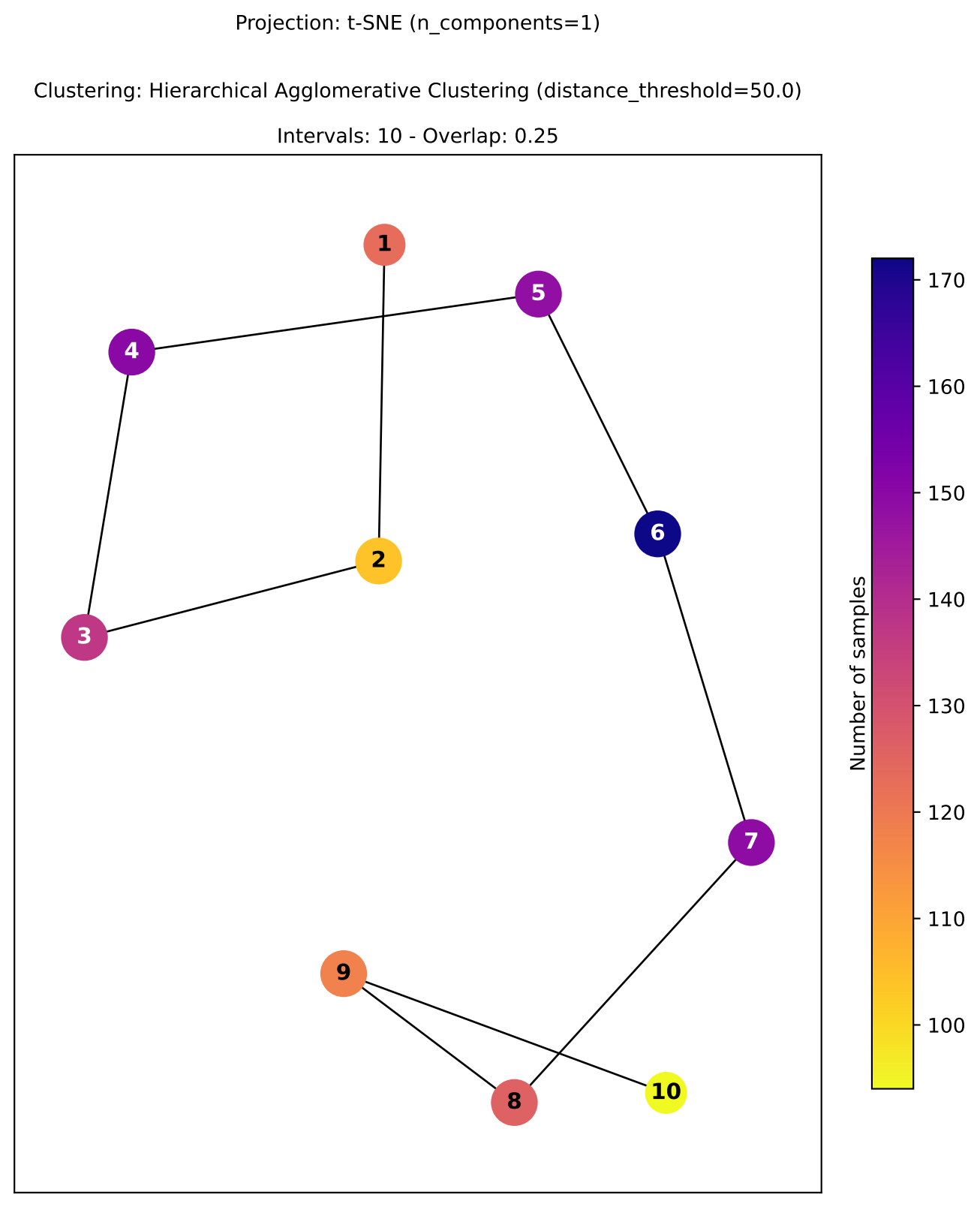
Projection: t-SNE (n_components=1)
Clustering: Hierarchical Agglomerative Clustering (distance_threshold=50.0)
Intervals: 10 - Overlap: 0.25
1
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Number of samples
170
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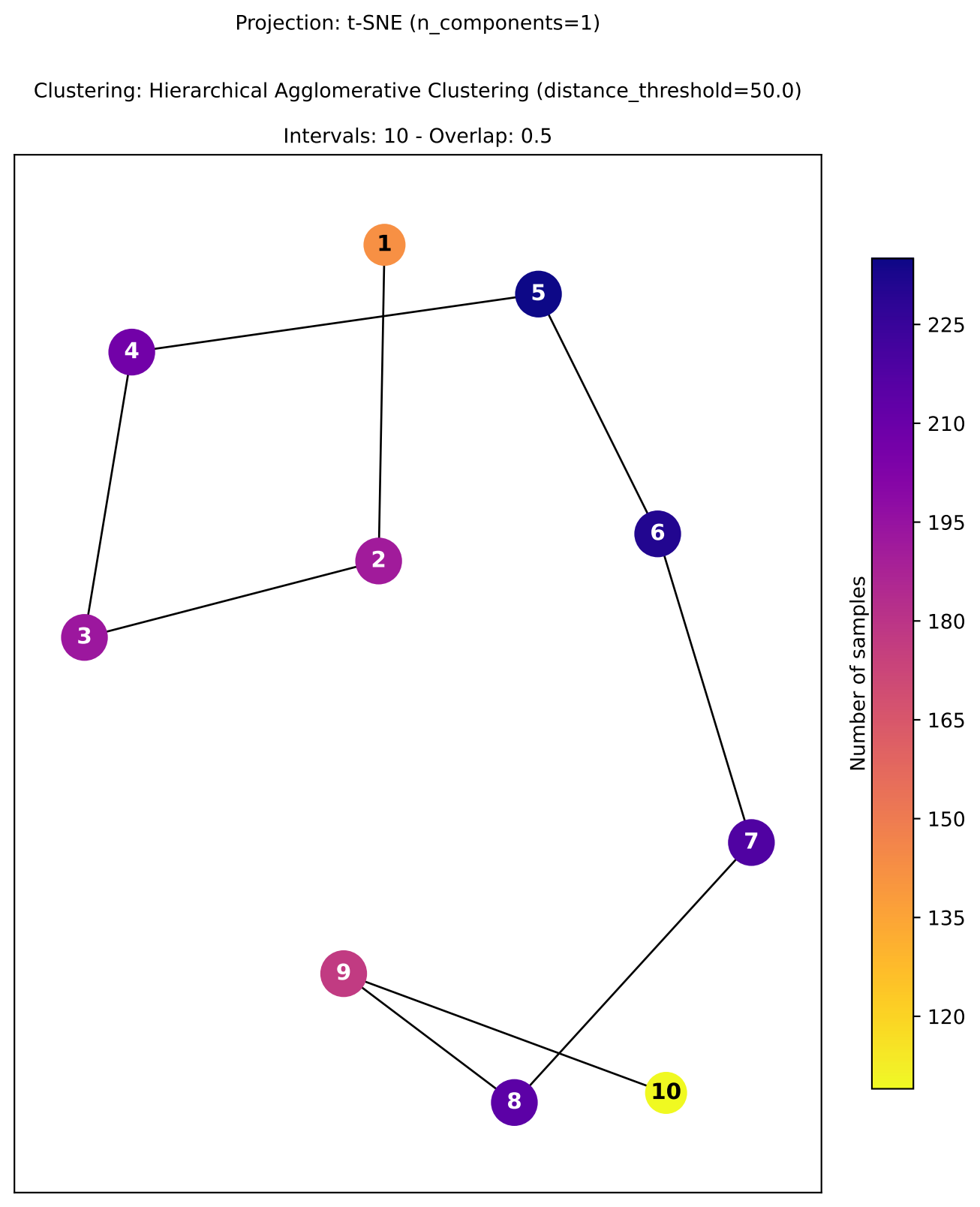
Projection: t-SNE (n_components=1)
Clustering: Hierarchical Agglomerative Clustering (distance_threshold=50.0)
Intervals: 10 - Overlap: 0.5
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Number of samples
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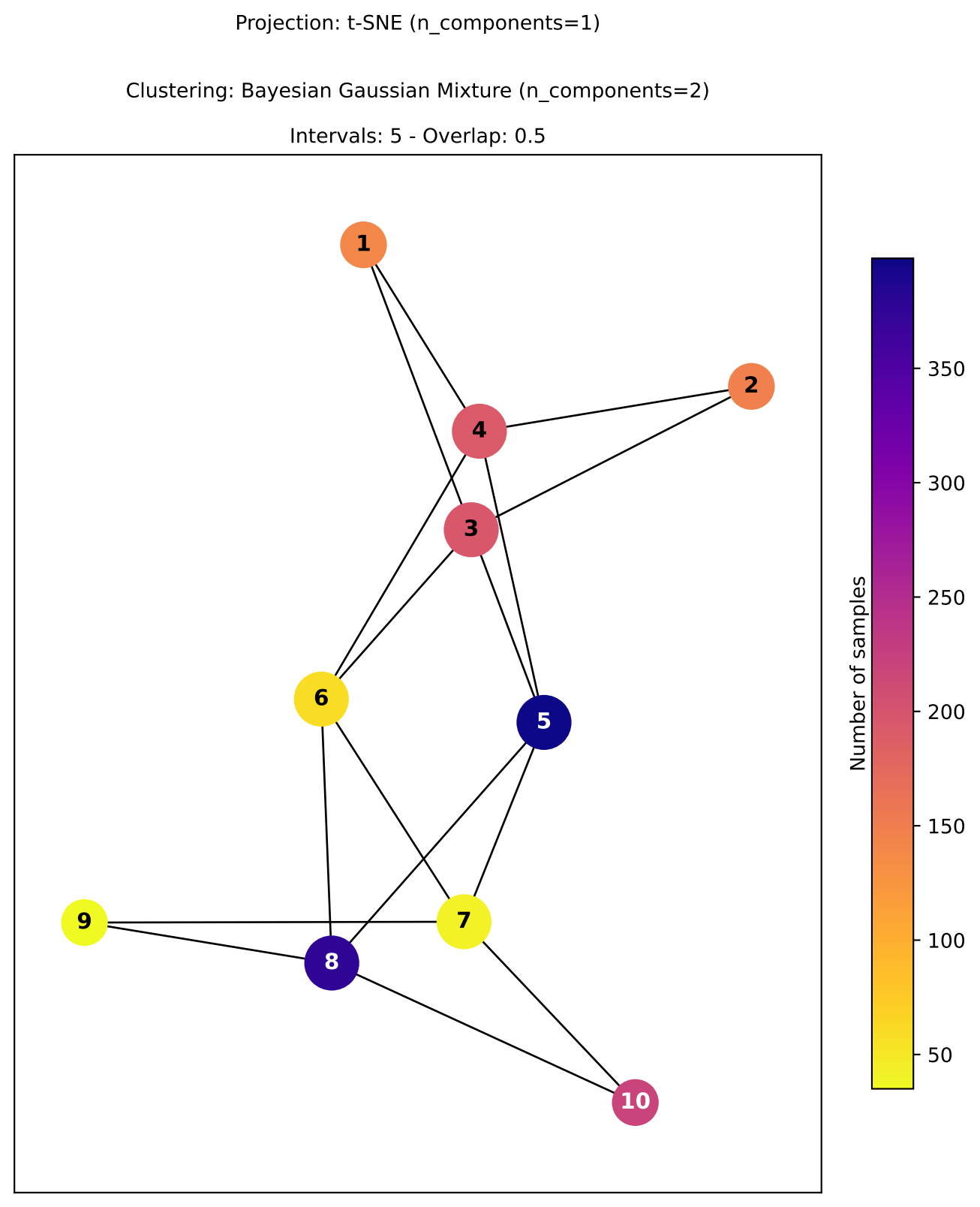
Projection: t-SNE (n_components=1)
Clustering: Bayesian Gaussian Mixture (n_components=2)
Intervals: 5 - Overlap: 0.5
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Number of samples
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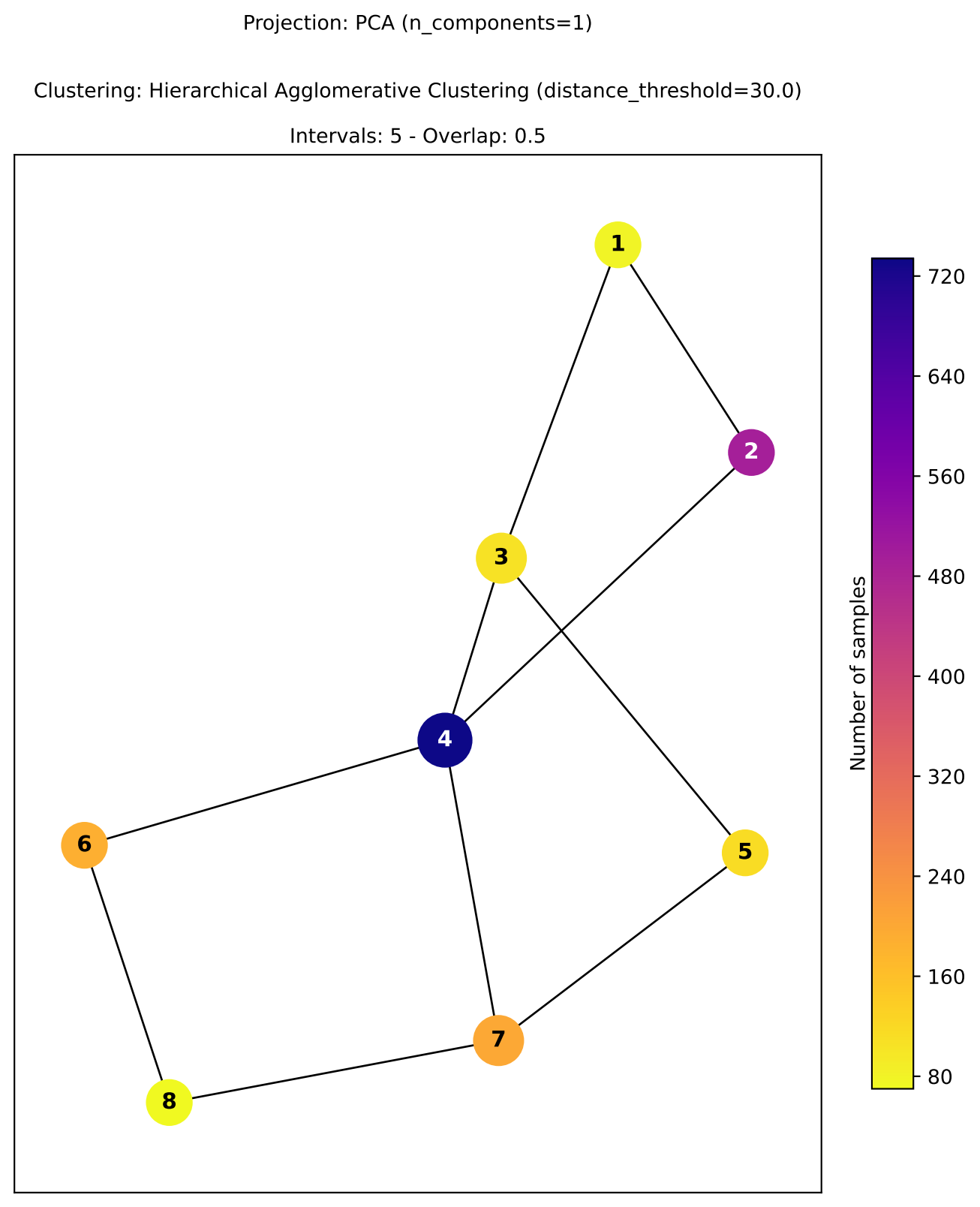
Projection: PCA (n_components=1)
Clustering: Hierarchical Agglomerative Clustering (distance_threshold=30.0)
Intervals: 5 - Overlap: 0.5
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Number of samples
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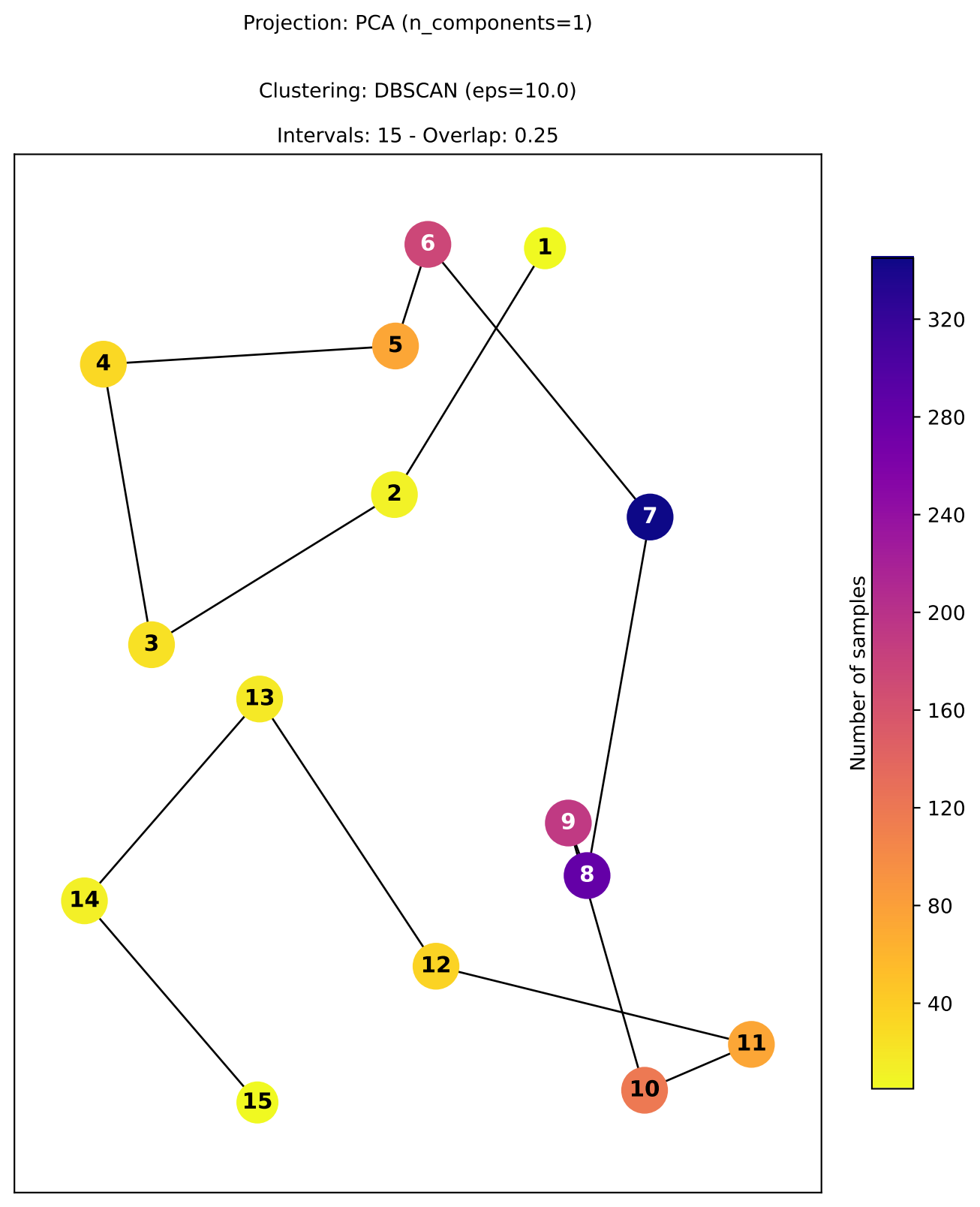
Projection: PCA (n_components=1)
Clustering: DBSCAN (eps=10.0)
Intervals: 15 - Overlap: 0.25
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Number of samples
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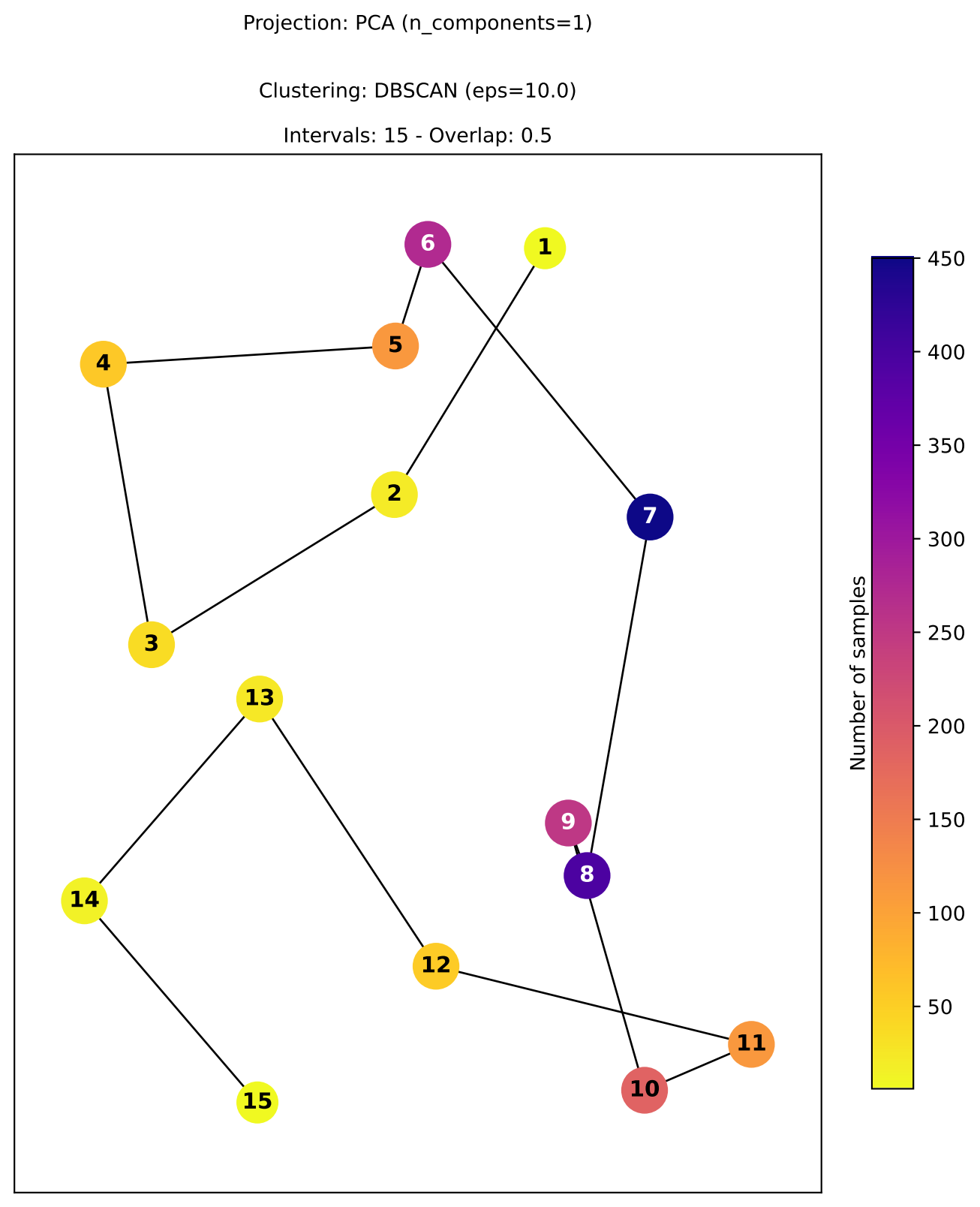
Projection: PCA (n_components=1)
Clustering: DBSCAN (eps=10.0)
Intervals: 15 - Overlap: 0.5
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Number of samples
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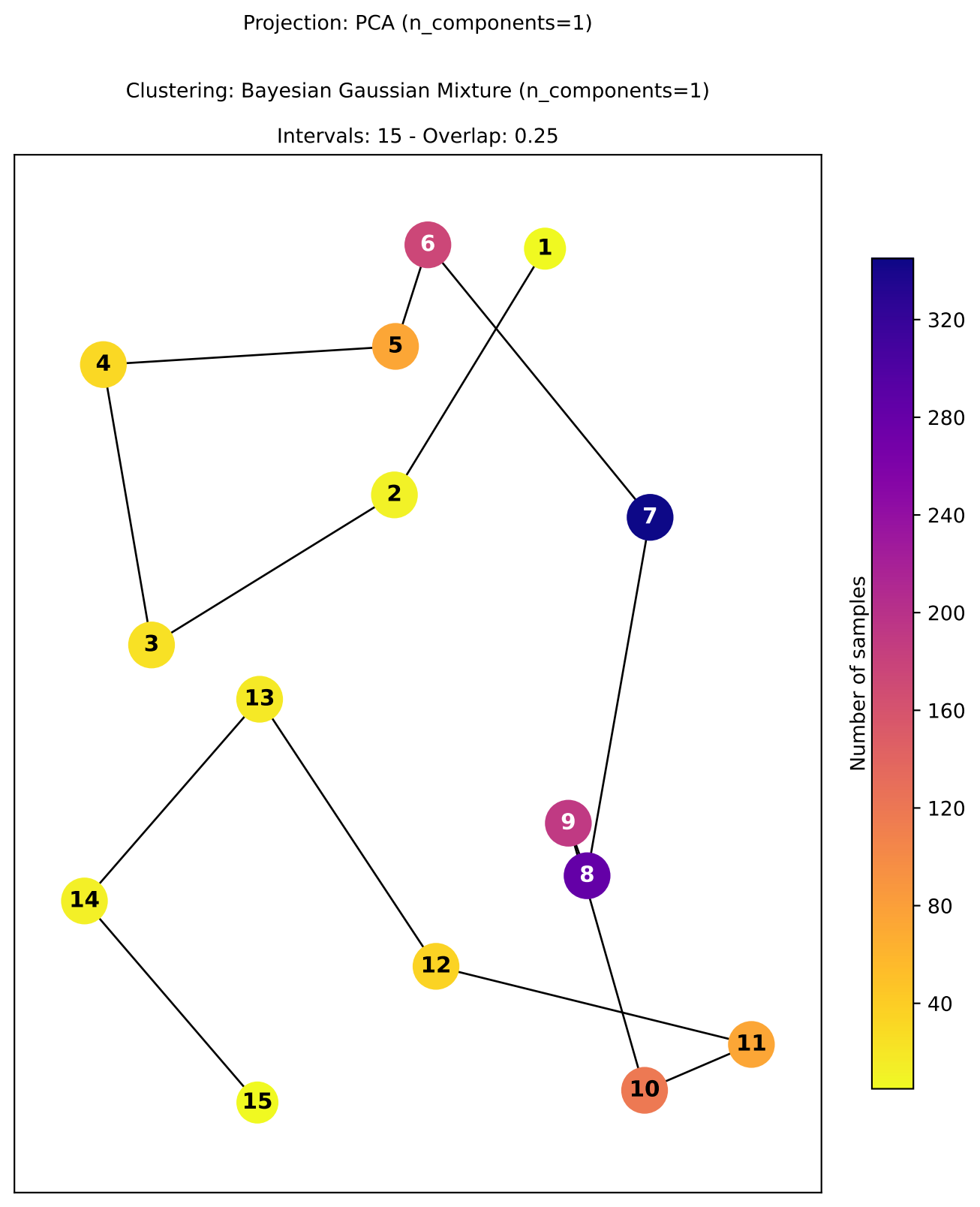
Projection: PCA (n_components=1)
Clustering: Bayesian Gaussian Mixture (n_components=1)
Intervals: 15 - Overlap: 0.25
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Number of samples
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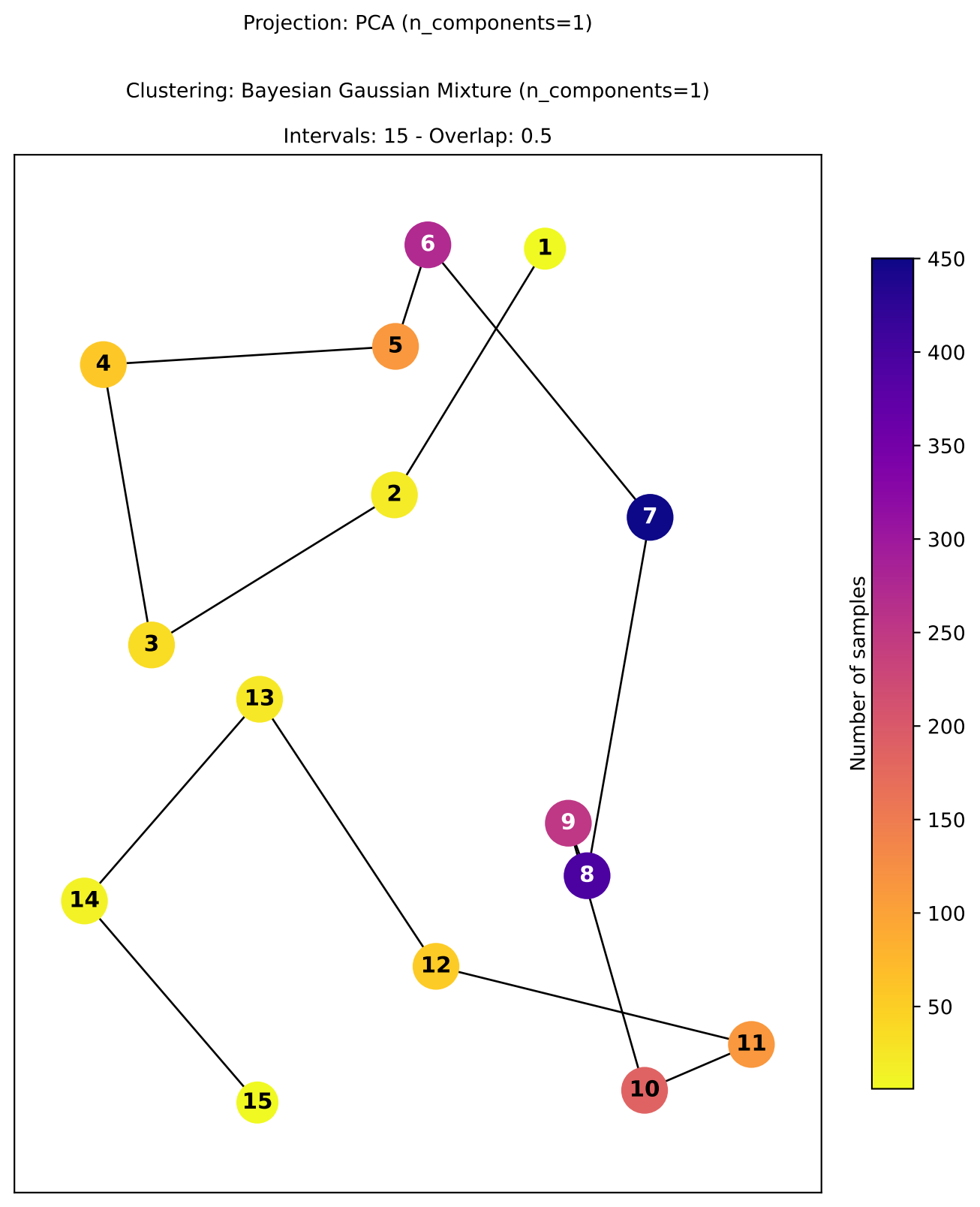
Projection: PCA (n_components=1)
Clustering: Bayesian Gaussian Mixture (n_components=1)
Intervals: 15 - Overlap: 0.5
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Number of samples
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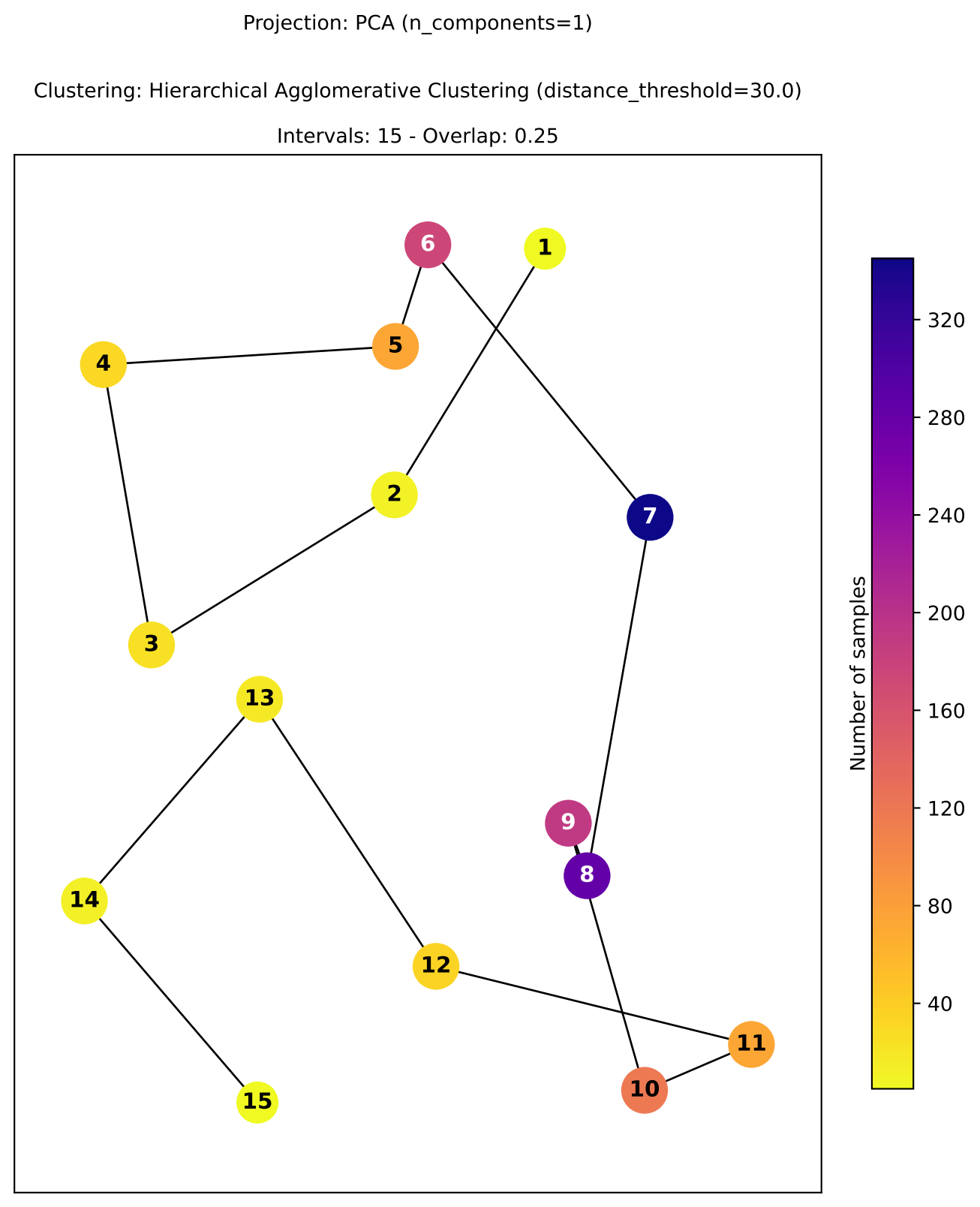
Projection: PCA (n_components=1)
Clustering: Hierarchical Agglomerative Clustering (distance_threshold=30.0)
Intervals: 15 - Overlap: 0.25
6
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Number of samples
320
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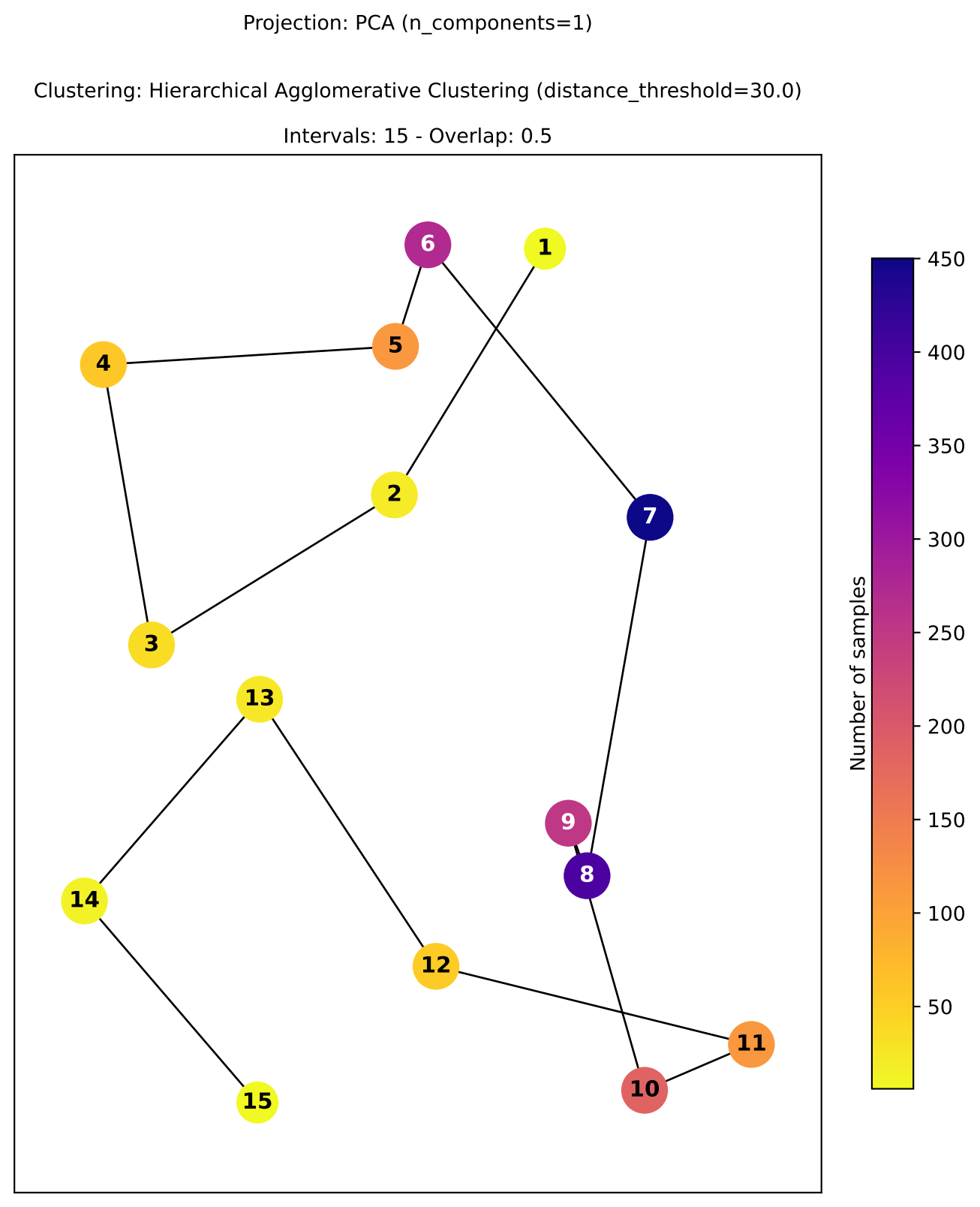
80
40


Projection: PCA (n_components=1)
Clustering: Hierarchical Agglomerative Clustering (distance_threshold=30.0)
Intervals: 15 - Overlap: 0.5
6
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13
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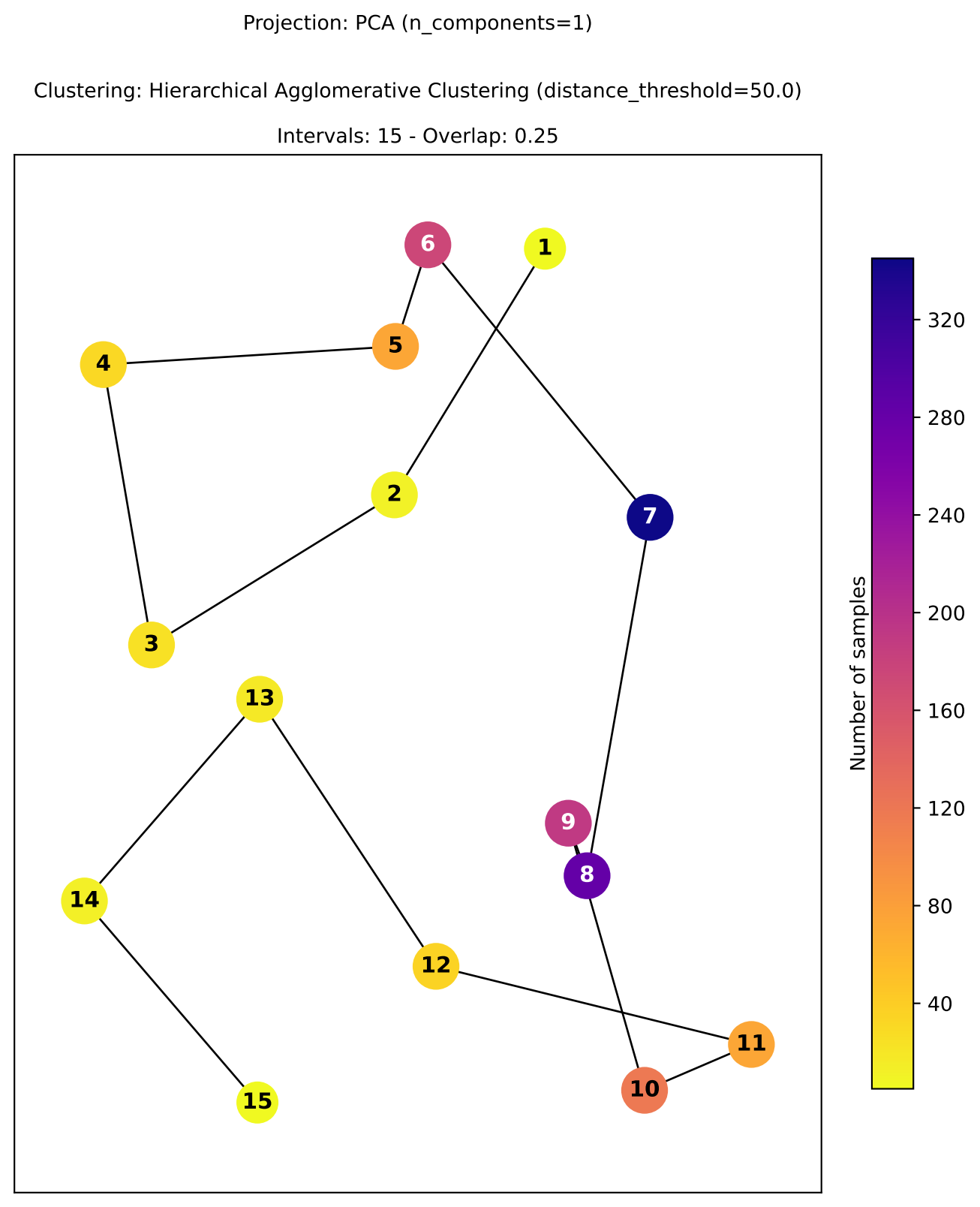
8
14
12
11
10
15
Number of samples
450
400
350
300
250
200
150
100
50


Projection: PCA (n_components=1)
Clustering: Hierarchical Agglomerative Clustering (distance_threshold=50.0)
Intervals: 15 - Overlap: 0.25
6
1
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9
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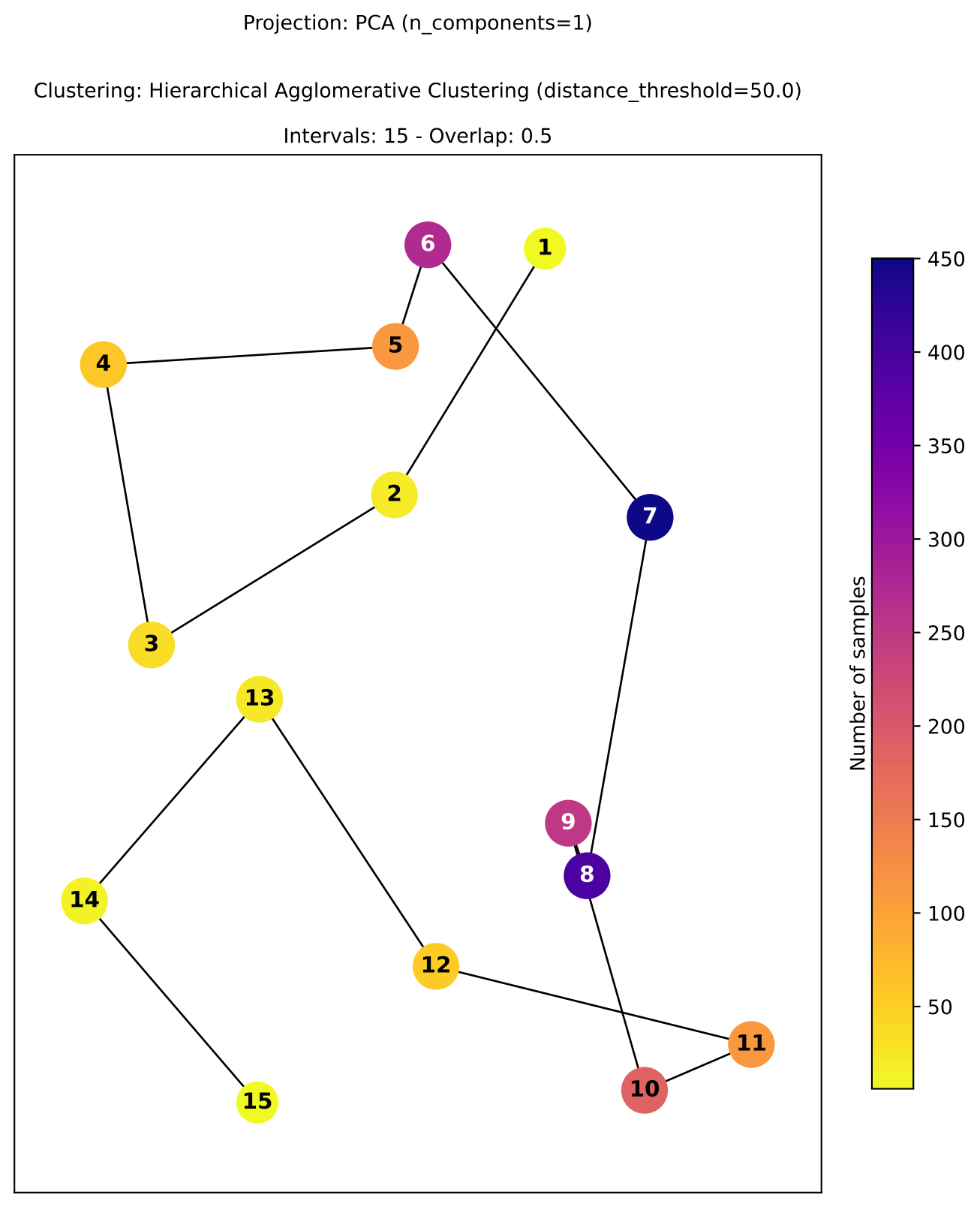
14
12
11
10
15
Number of samples
320
280
240
200
160
120
80
40


Projection: PCA (n_components=1)
Clustering: Hierarchical Agglomerative Clustering (distance_threshold=50.0)
Intervals: 15 - Overlap: 0.5
6
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8
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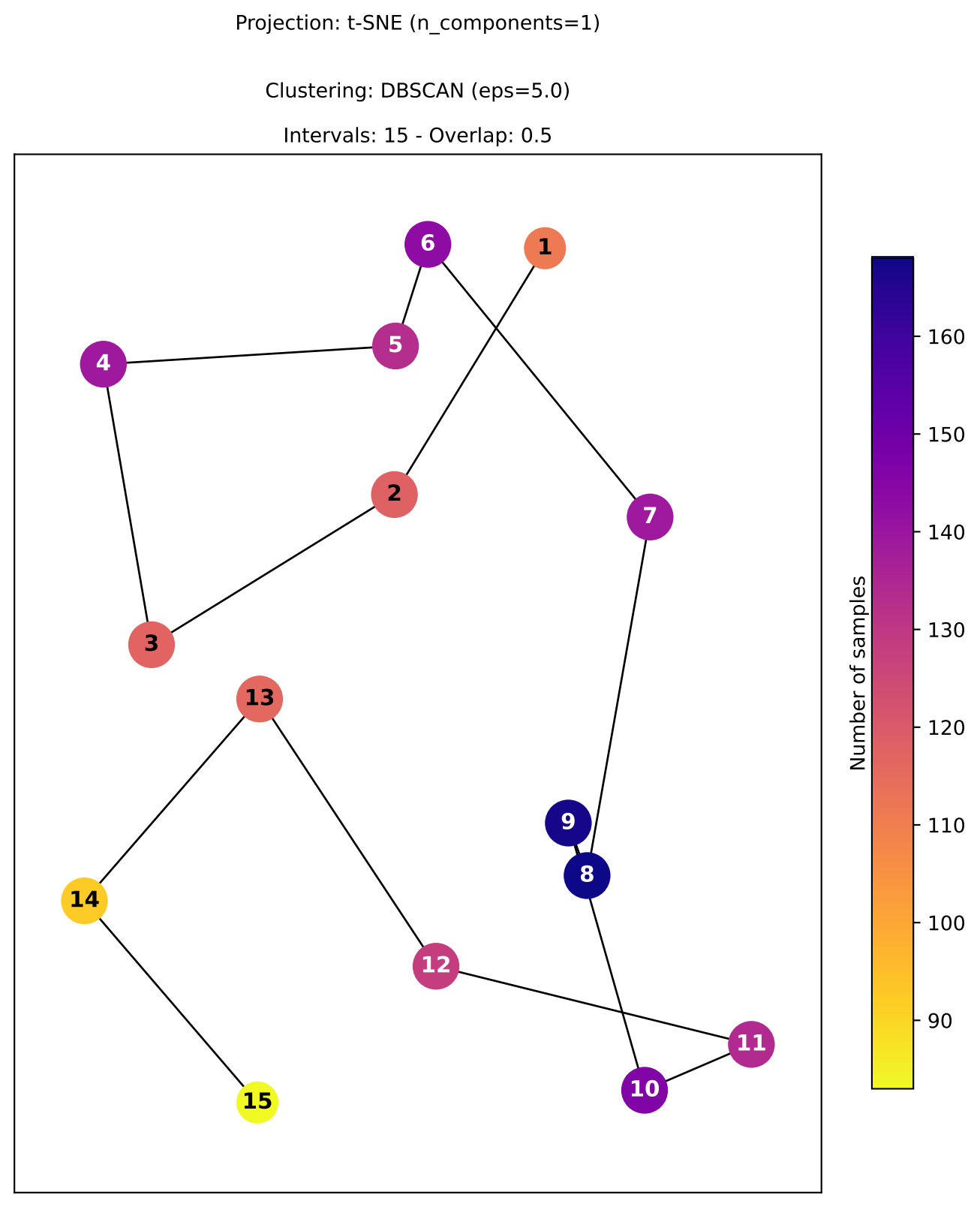
15
Number of samples
450
400
350
300
250
200
150
100
50


Projection: t-SNE (n_components=1)
Clustering: DBSCAN (eps=5.0)
Intervals: 15 - Overlap: 0.5
6
1
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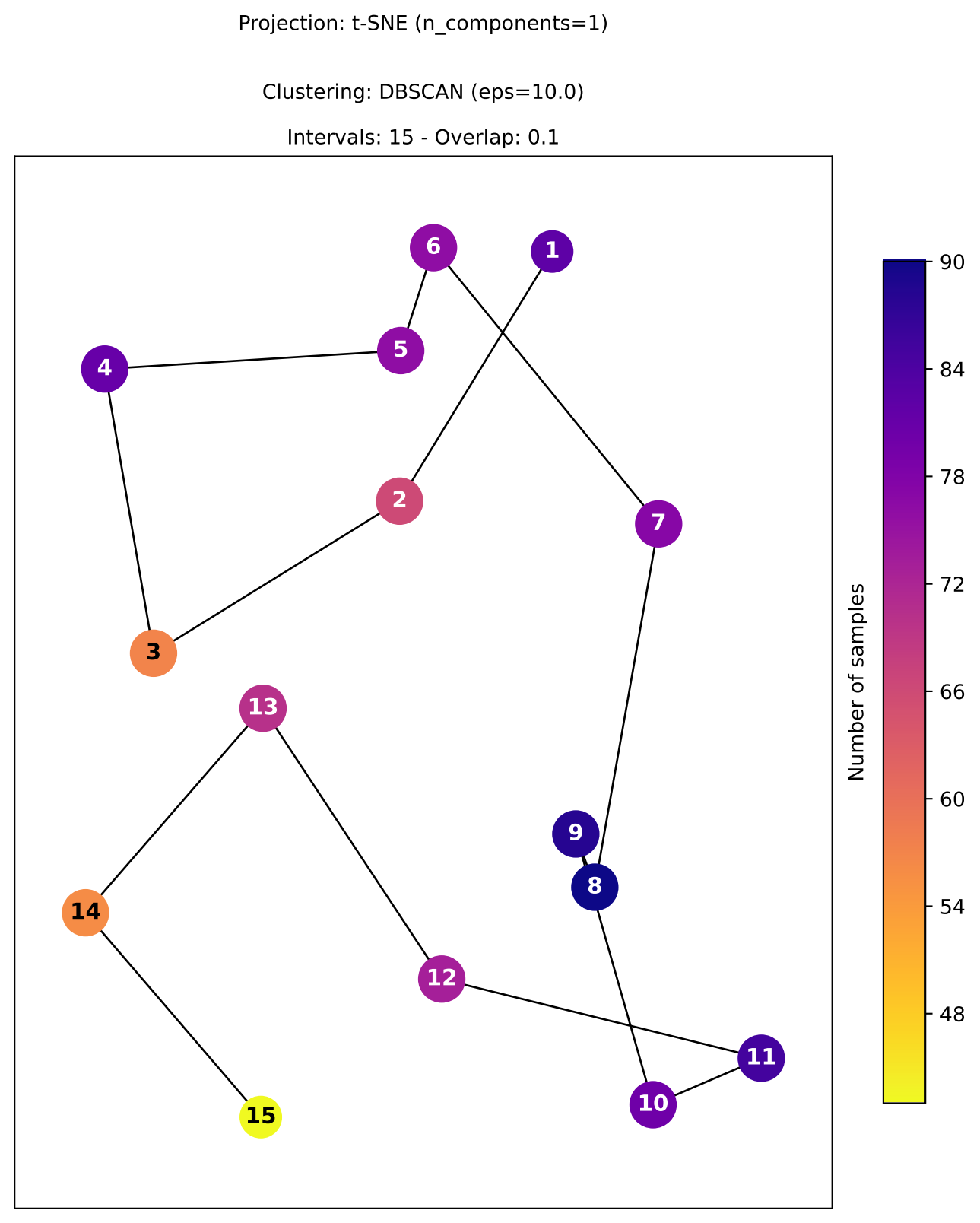
13
9
8
14
12
11
10
15
Number of samples
160
150
140
130
120
110
100
90


Projection: t-SNE (n_components=1)
Clustering: DBSCAN (eps=10.0)
Intervals: 15 - Overlap: 0.1
6
1
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4
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7
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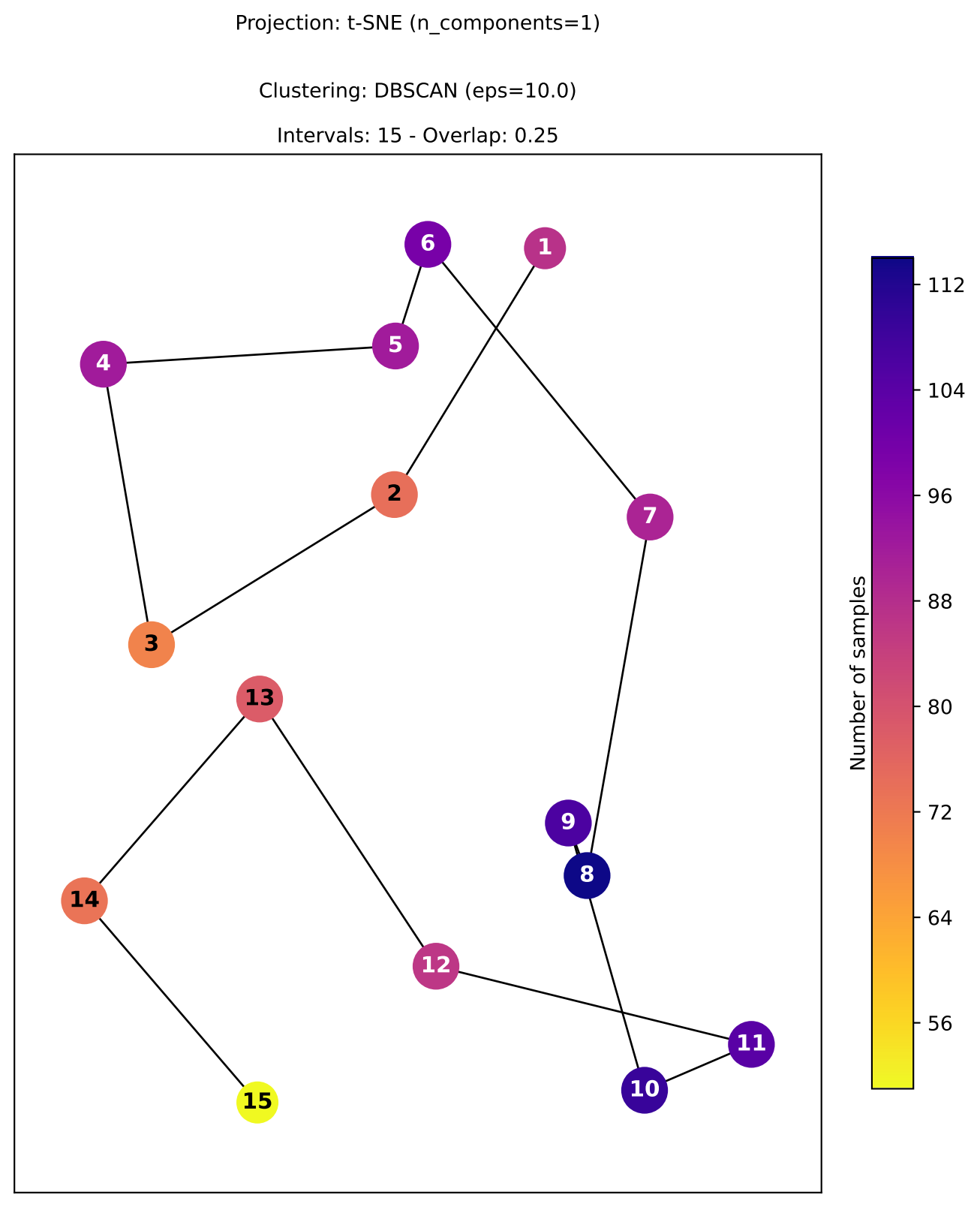
9
8
14
12
11
10
15
Number of samples
90
84
78
72
66
60
54
48


Projection: t-SNE (n_components=1)
Clustering: DBSCAN (eps=10.0)
Intervals: 15 - Overlap: 0.25
6
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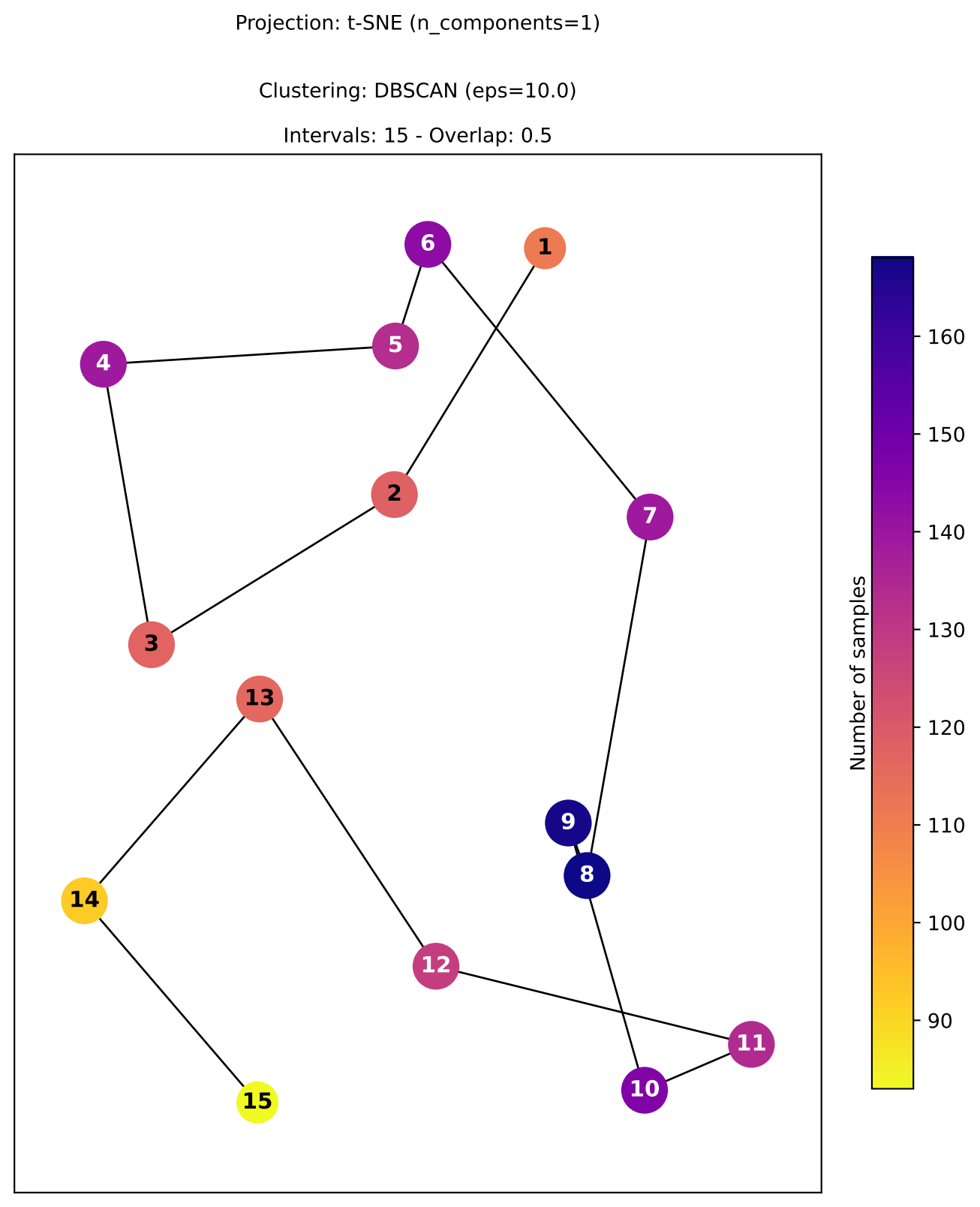
15
Number of samples
112
104
96
88
80
72
64
56


Projection: t-SNE (n_components=1)
Clustering: DBSCAN (eps=10.0)
Intervals: 15 - Overlap: 0.5
6
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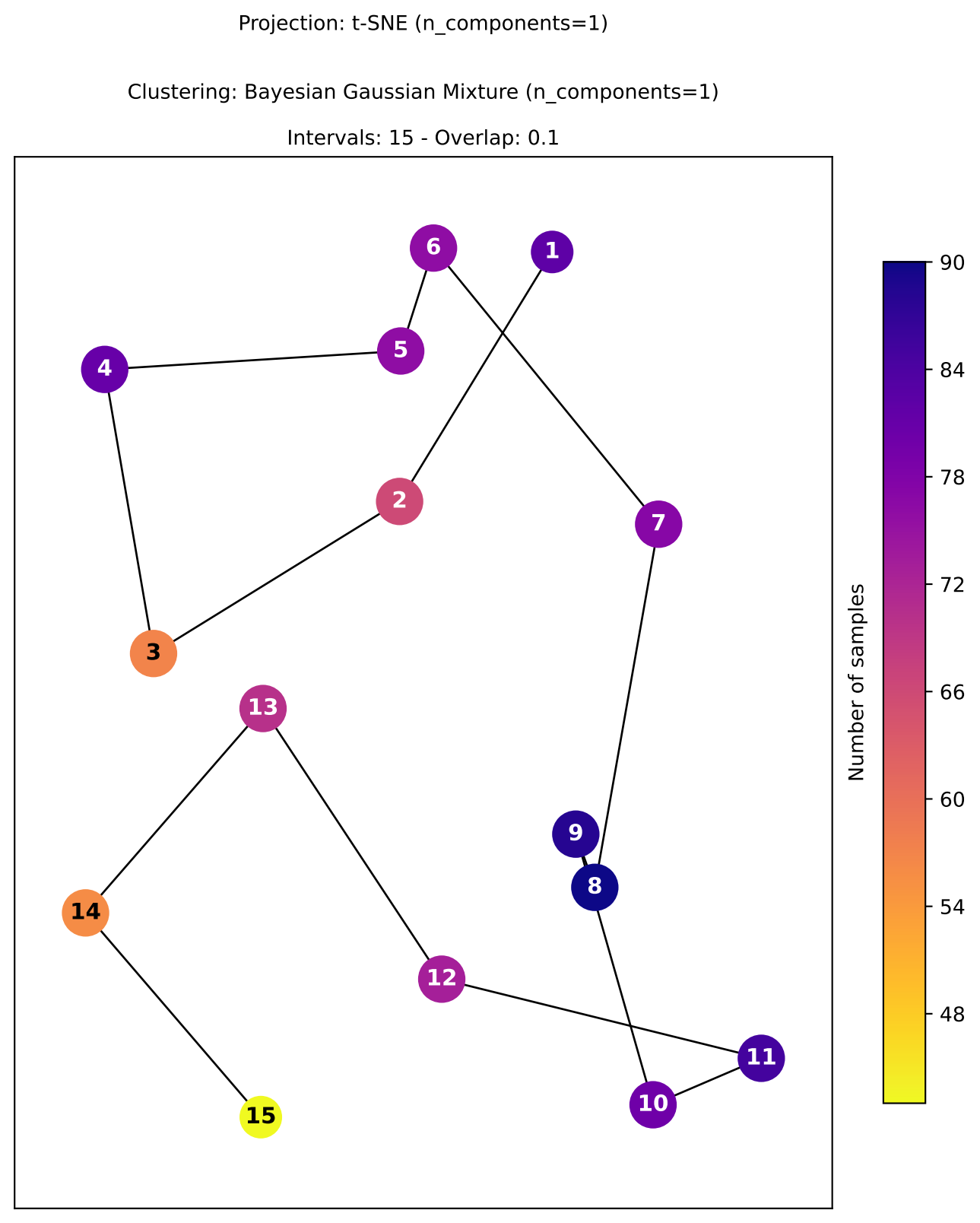
Number of samples
160
150
140
130
120
110
100
90


Projection: t-SNE (n_components=1)
Clustering: Bayesian Gaussian Mixture (n_components=1)
Intervals: 15 - Overlap: 0.1
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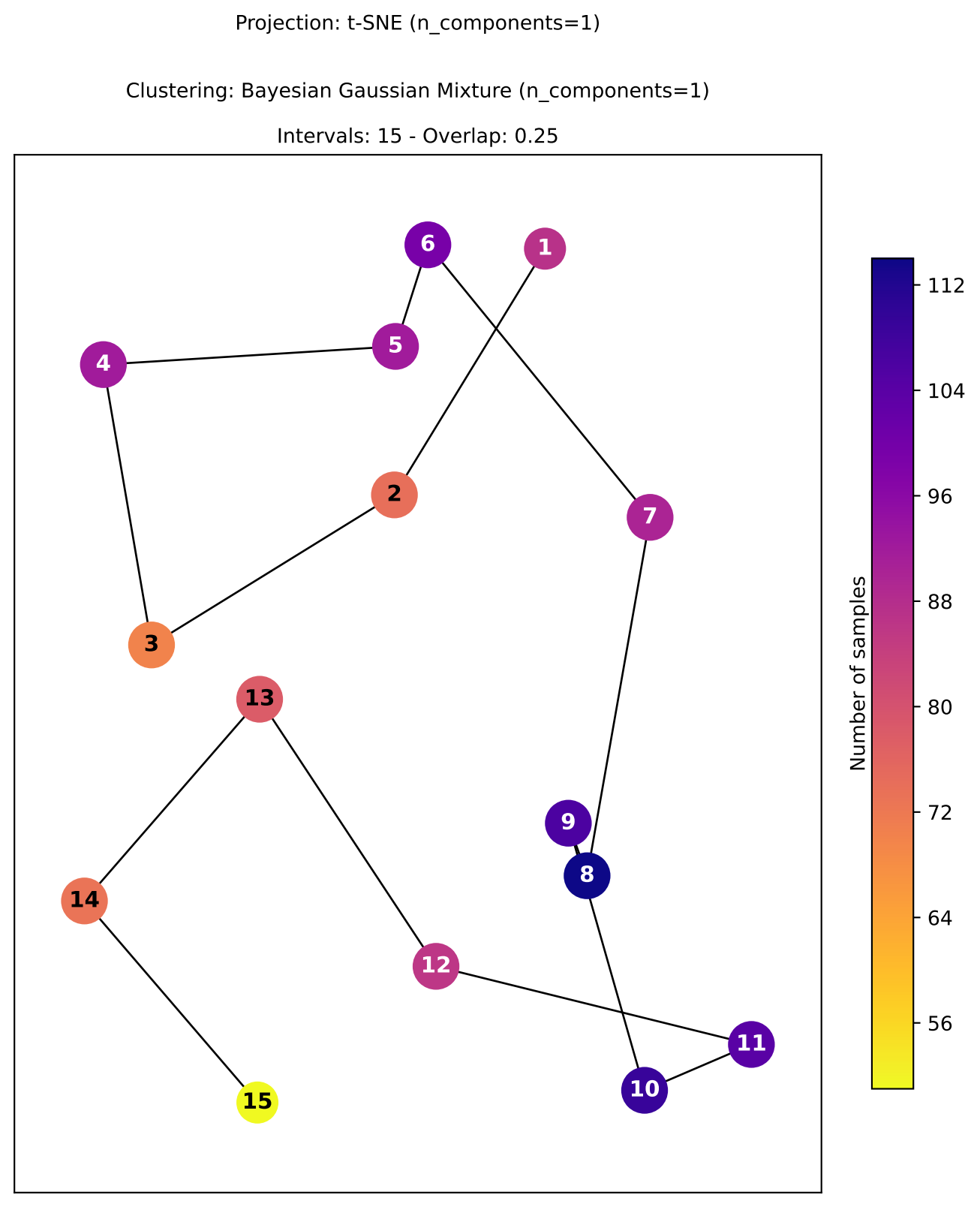
Number of samples
90
84
78
72
66
60
54
48


Projection: t-SNE (n_components=1)
Clustering: Bayesian Gaussian Mixture (n_components=1)
Intervals: 15 - Overlap: 0.25
6
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Number of samples
112
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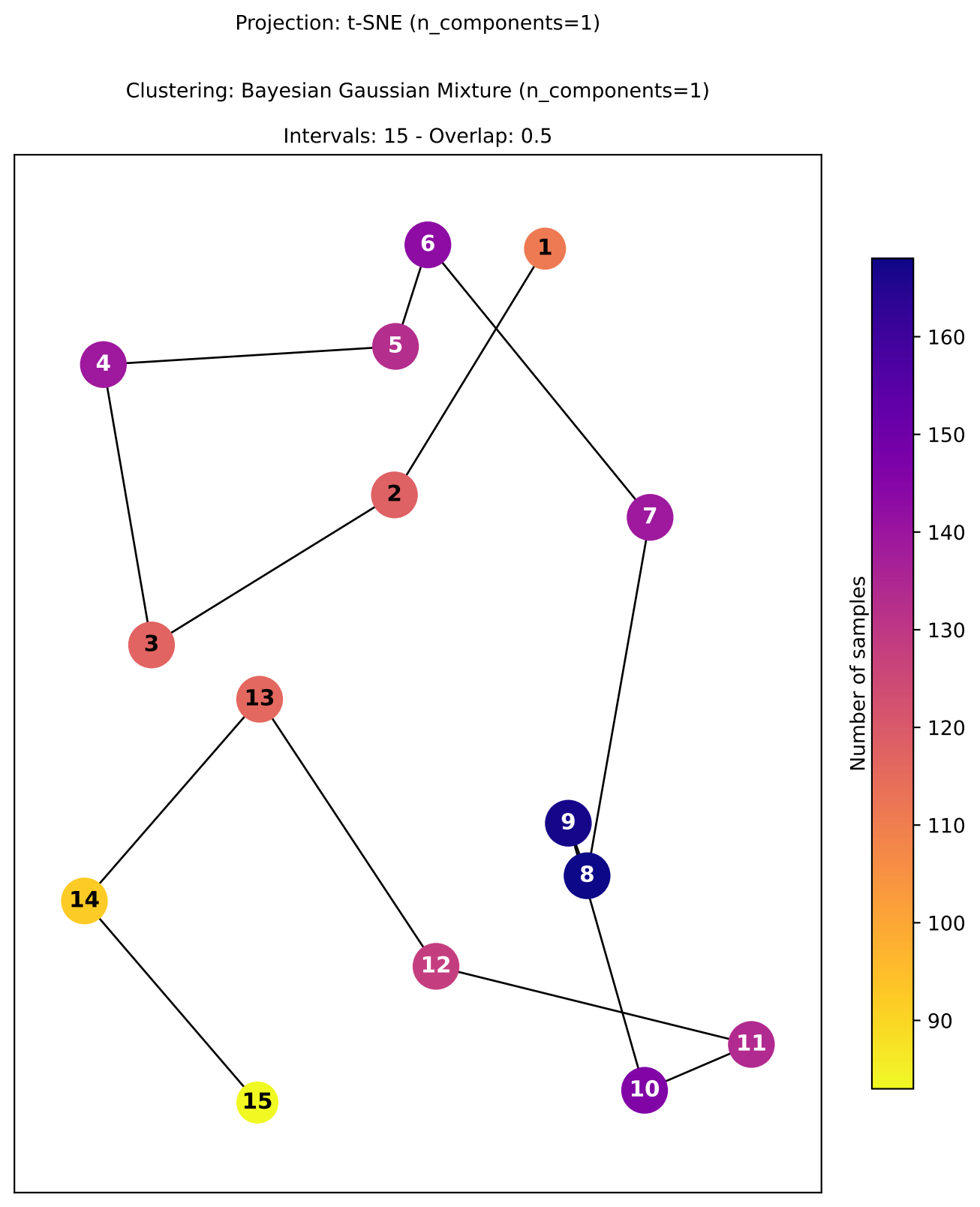
80
72
64
56


Projection: t-SNE (n_components=1)
Clustering: Bayesian Gaussian Mixture (n_components=1)
Intervals: 15 - Overlap: 0.5
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Number of samples
160
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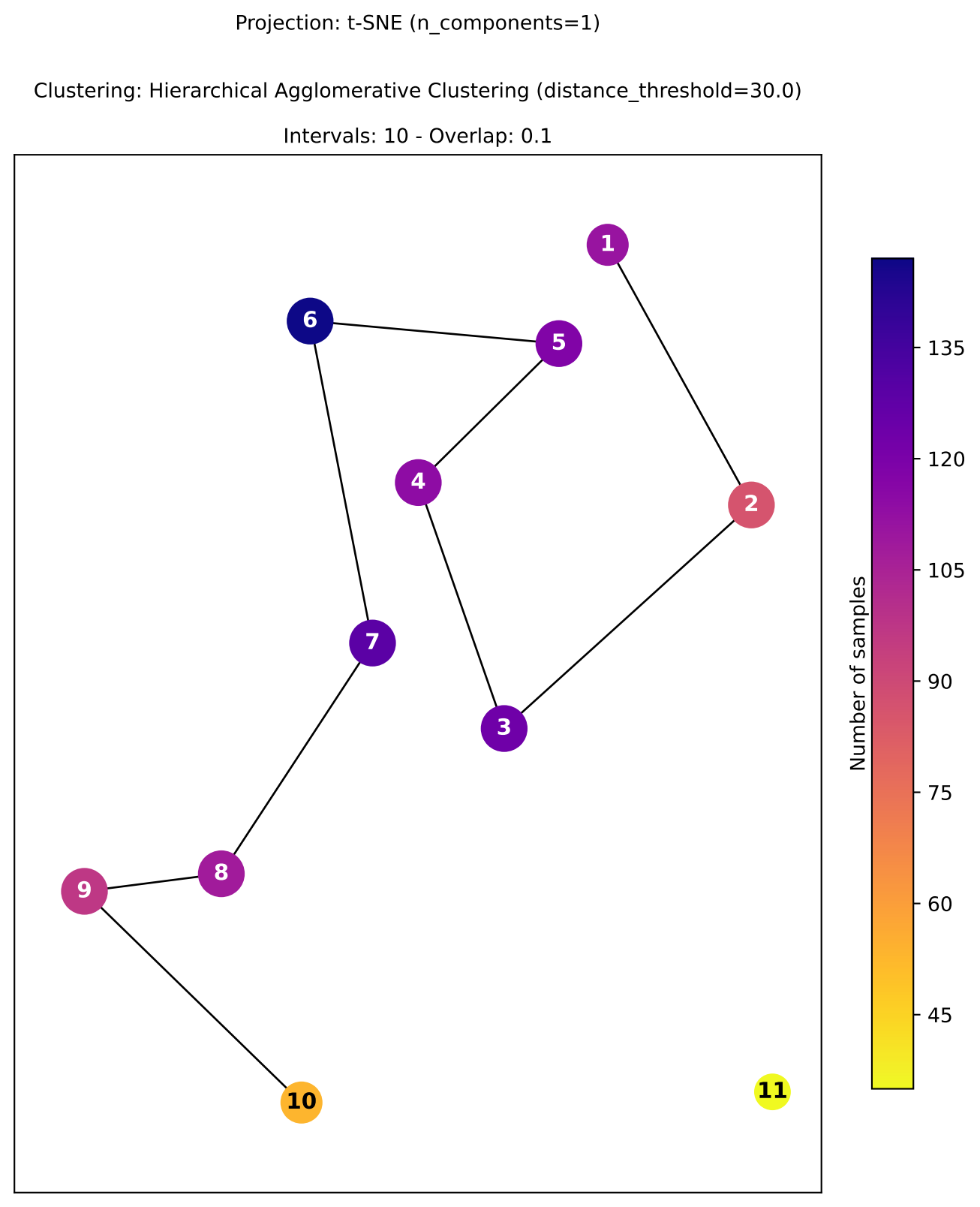
Projection: t-SNE (n_components=1)
Clustering: Hierarchical Agglomerative Clustering (distance_threshold=30.0)
Intervals: 10 - Overlap: 0.1
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6
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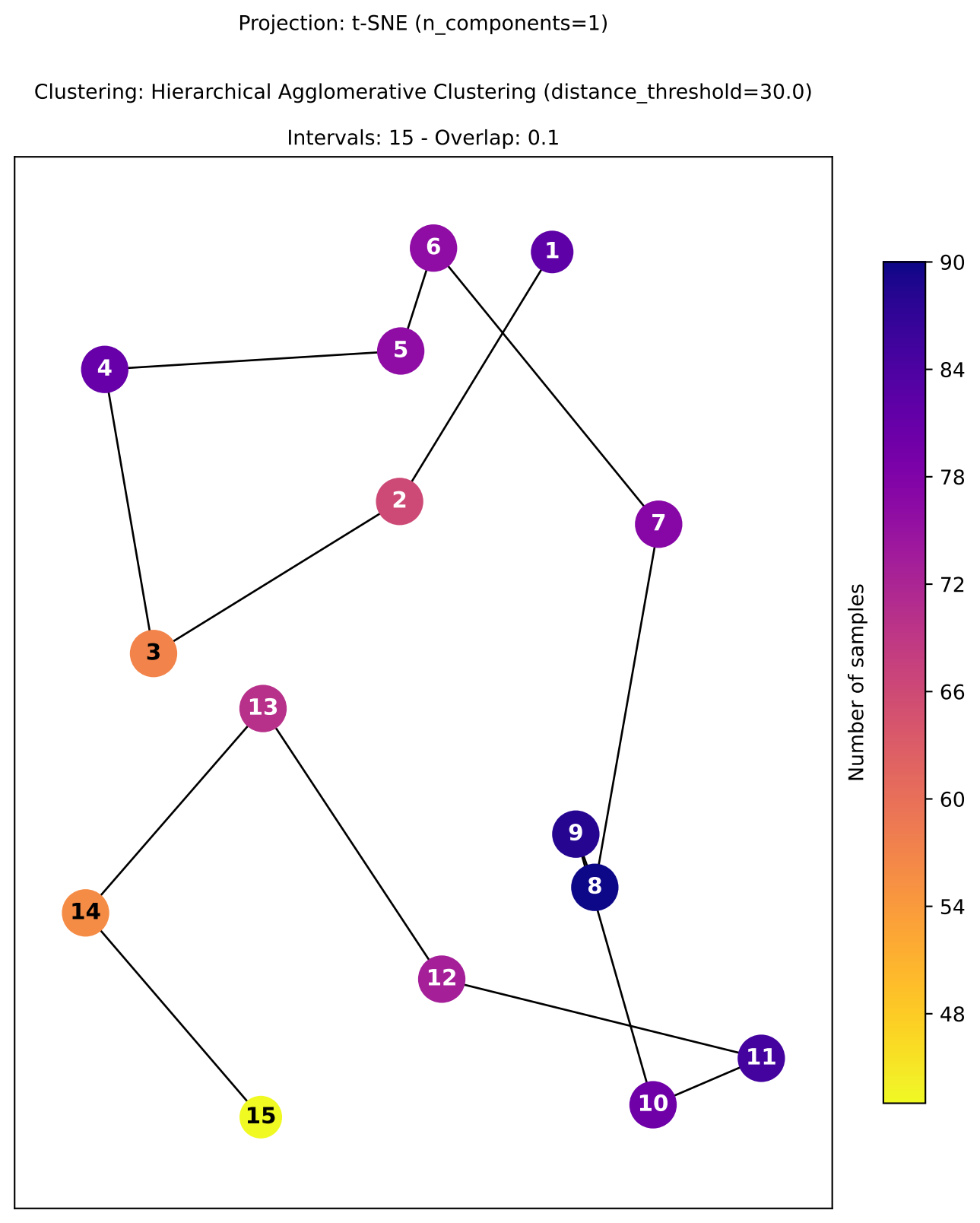
11
Number of samples
135
120
105
90
75
60
45


Projection: t-SNE (n_components=1)
Clustering: Hierarchical Agglomerative Clustering (distance_threshold=30.0)
Intervals: 15 - Overlap: 0.1
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Number of samples
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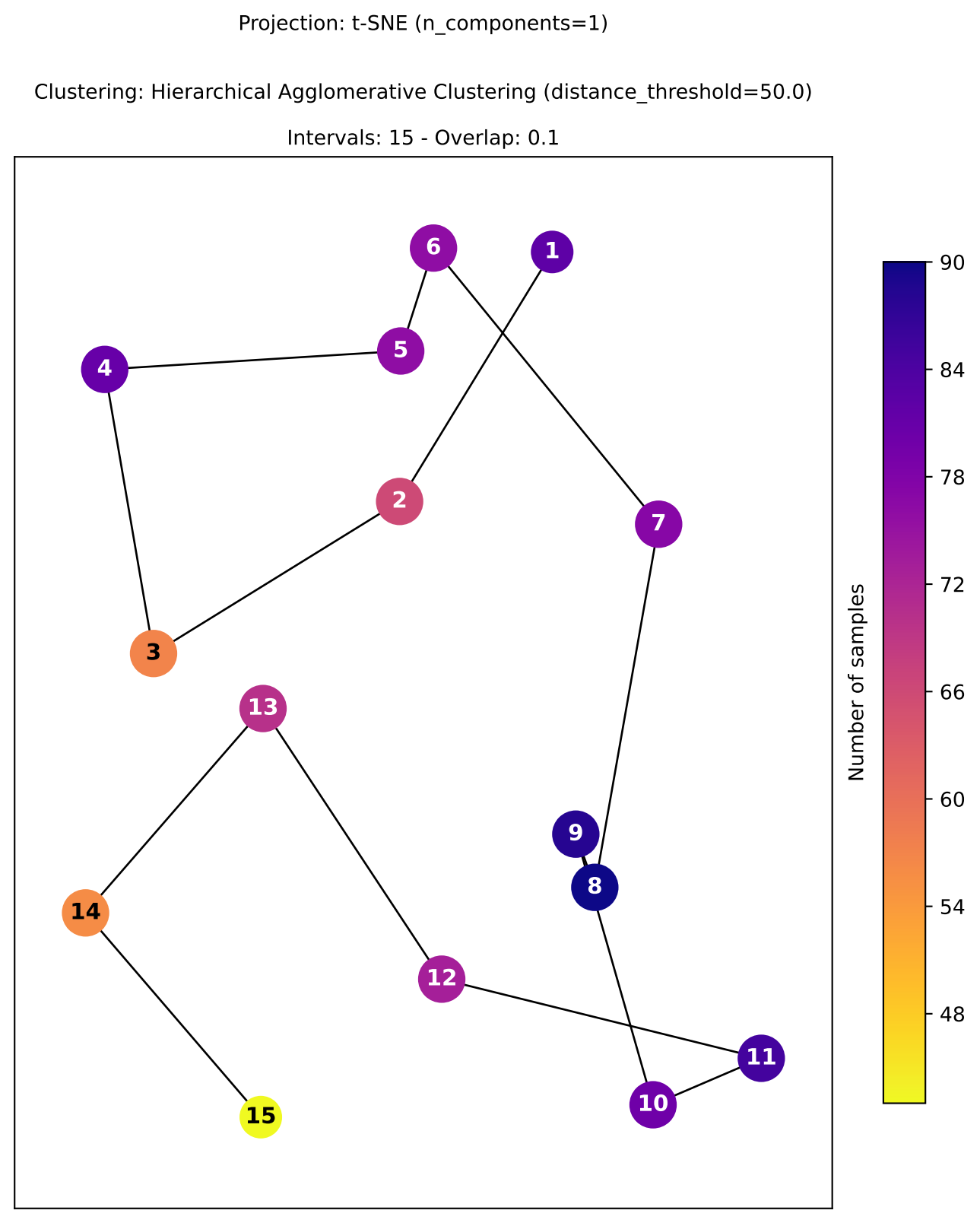
Projection: t-SNE (n_components=1)
Clustering: Hierarchical Agglomerative Clustering (distance_threshold=50.0)
Intervals: 15 - Overlap: 0.1
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Number of samples
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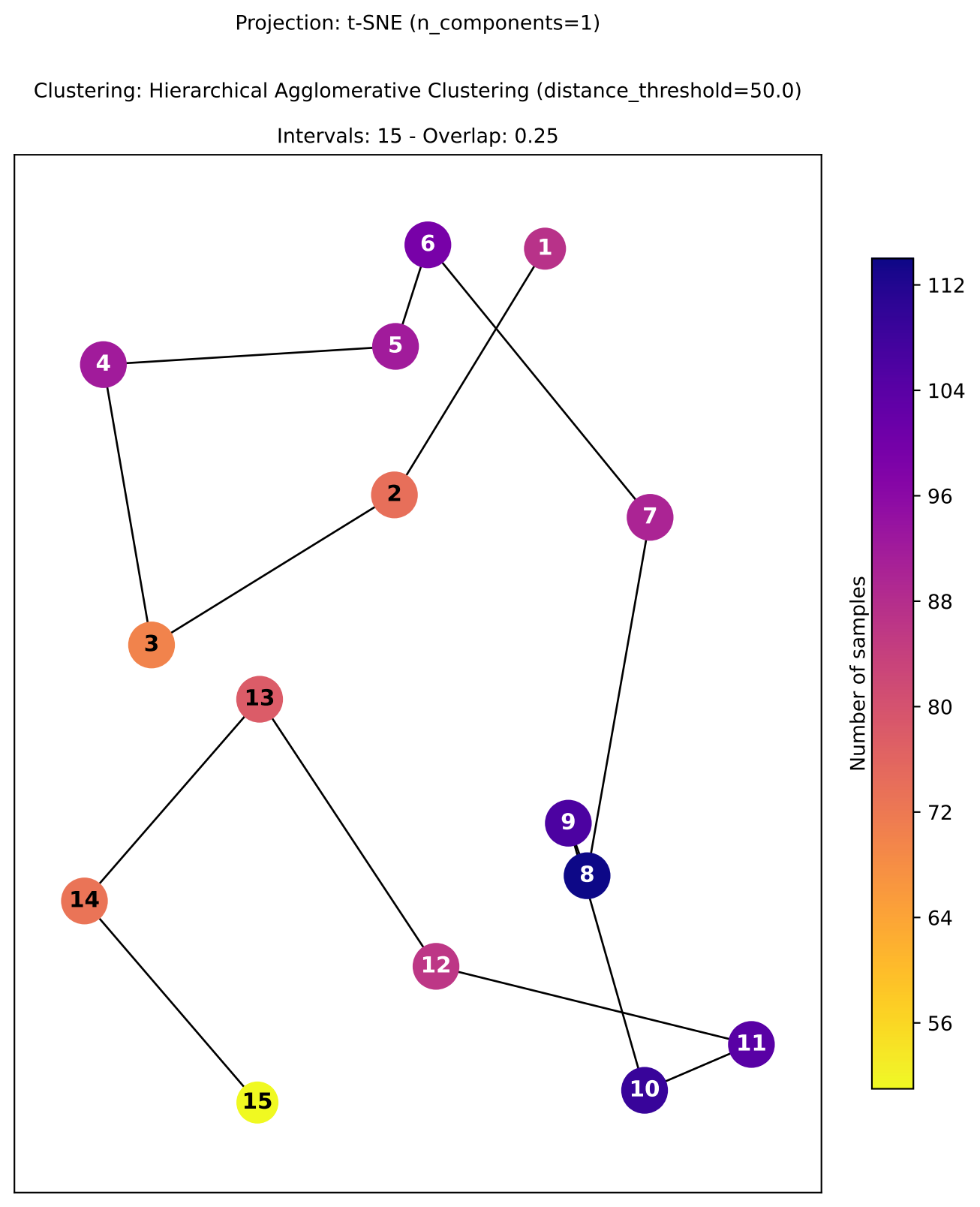
Projection: t-SNE (n_components=1)
Clustering: Hierarchical Agglomerative Clustering (distance_threshold=50.0)
Intervals: 15 - Overlap: 0.25
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Number of samples
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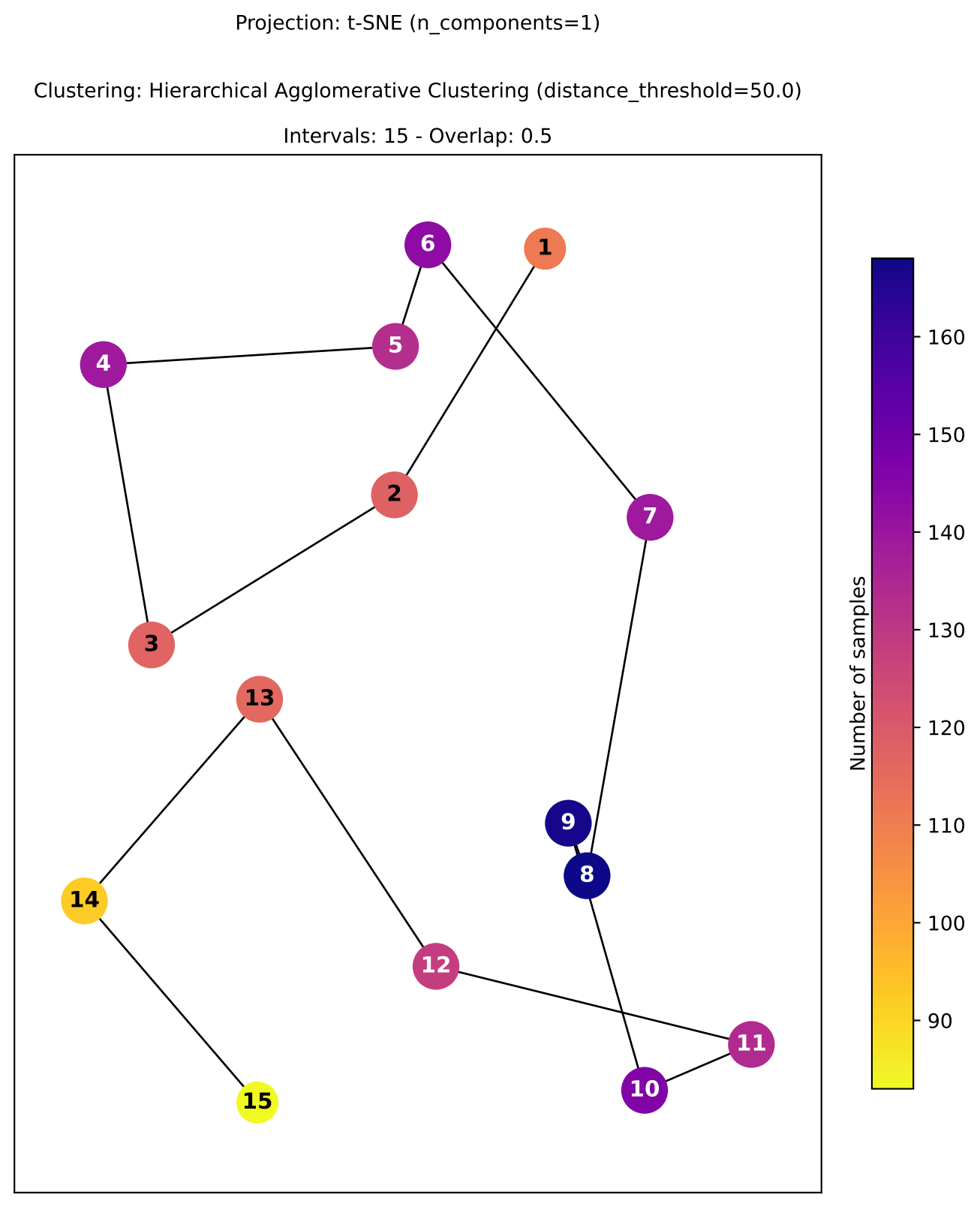
Projection: t-SNE (n_components=1)
Clustering: Hierarchical Agglomerative Clustering (distance_threshold=50.0)
Intervals: 15 - Overlap: 0.5
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Number of samples
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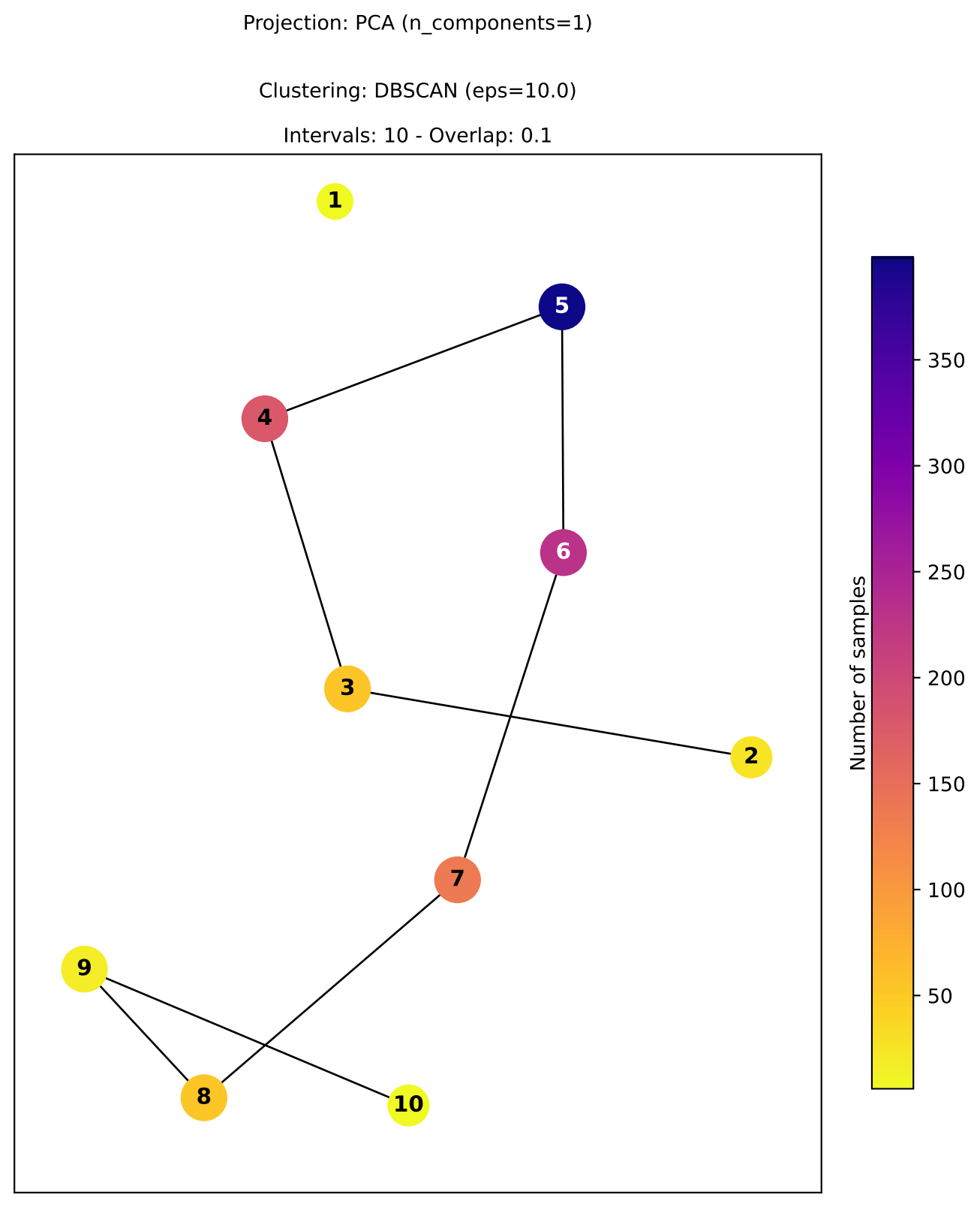
Projection: PCA (n_components=1)
Clustering: DBSCAN (eps=10.0)
Intervals: 10 - Overlap: 0.1
1
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Number of samples
350
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200
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100
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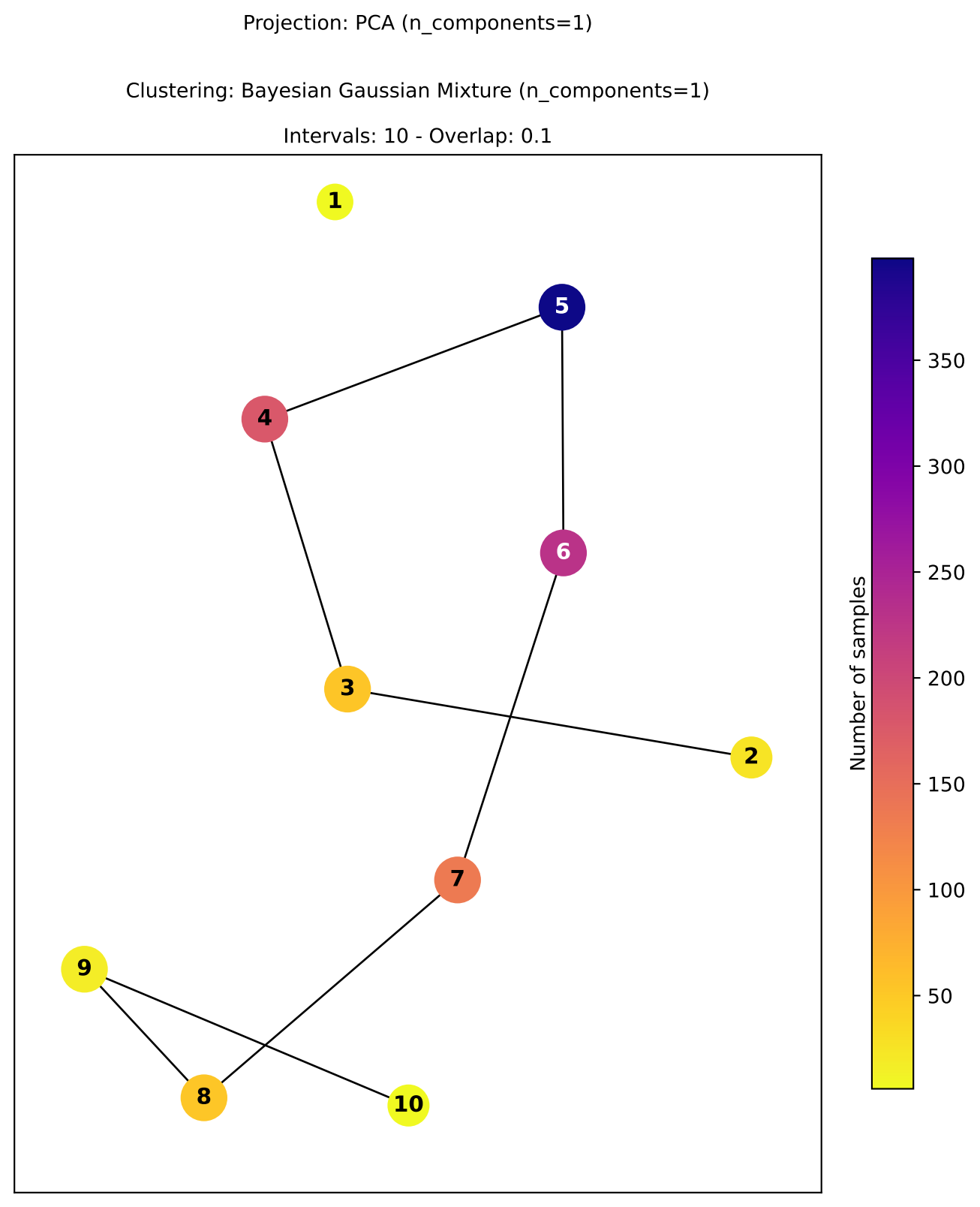
Projection: PCA (n_components=1)
Clustering: Bayesian Gaussian Mixture (n_components=1)
Intervals: 10 - Overlap: 0.1
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Number of samples
350
300
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